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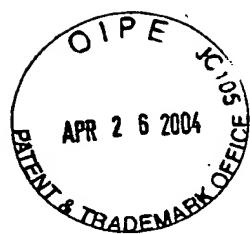
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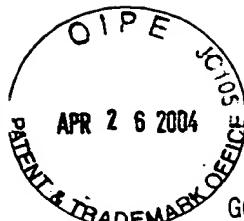
|  |     |
|--|-----|
| ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG | 60  |
| MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu | 20  |
| GTGCTGCCGCTGGCCACGTTCGTGGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG  | 120 |
| ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln | 40  |
| CGCGGGGACCCGGCGGCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCTGG   | 180 |
| ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp | 60  |
| GACGCACGGCCGCCCGCCGCCCTCCTCCGCCAGGTGTCCTGCCTGAAGGAGCTG       | 240 |
| AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 80  |
| GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGAAGAACGTGCTGGCCTCGC    | 300 |
| ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly | 100 |
| TTCGCGCTGGACGGGCCGCGGGGCCCCGAGGCCTTCACCCACCAGCGTGC           | 360 |
| PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg | 120 |
| AGCTACCTGCCAACACGGTGACCGACGCACGTGGGGGAGCGGGCGTGGGGCTGCTG     | 420 |
| SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu | 140 |
| TTGCGCCGCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTTTGTG    | 480 |
| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal | 160 |
| CTGGTGGCTCCAGCTGCGCCTACCAGGTGCGGGCCGCGCTGTACCAAGCTCGCGCT     | 540 |
| LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 180 |
| GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCGAAGGCGTGGGATGCGAA      | 600 |
| AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu    | 200 |
| CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCCTGCCAGCCCCGGT   | 660 |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 220 |
| GCGAGGAGGCAGGGGGCAGTGCCAGGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT   | 720 |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 240 |

Fig. 1A



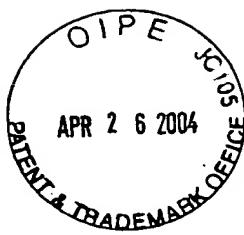
|   |      |
|---|------|
| GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGCTCTGGGCCACCCGGC        | 780  |
| GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly  | 260  |
| AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA    | 840  |
| ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu  | 280  |
| GAAGCCACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCCACCCATCCGTGGC         | 900  |
| GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly  | 300  |
| CGCCAGCACCGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCC      | 960  |
| ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro  | 320  |
| TGTCCCCCGGTGTACGCCAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG   | 1020 |
| CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln  | 340  |
| CTGCGGCCCTCTTCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC       | 1080 |
| LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu  | 360  |
| GTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCCCAGGTTGCC       | 1140 |
| ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro  | 380  |
| CGCCTGCCCAAGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC     | 1200 |
| ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis  | 400  |
| GCGCAGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCCGTCACC    | 1260 |
| AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr  | 420  |
| CCAGCAGCCGGTGTCTGCCCCGGAGAAGCCCCAGGGCTCTGTGGCGGCCCGAGGAG      | 1320 |
| ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu  | 440  |
| GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAG | 1380 |
| GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln  | 460  |
| GTGTACGGCTTCGTGCGGGCTGCCTGCCTGCCGGCTGGTGCCTGGGGCTCC           | 1440 |
| ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer  | 480  |
| AGGCACAAACGAACGCCGCTTCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGAAGCAT | 1500 |
| ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis  | 500  |

Fig. 1B



|  |             |
|--|-------------|
| GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTTGGCTG<br>AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 1560<br>520 |
| CGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC<br>ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle  | 1620<br>540 |
| CTGGCCAAGTTCCCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC<br>LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe      | 1680<br>560 |
| TTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTC<br>PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal          | 1740<br>580 |
| TGGAGCAAGTTGCAAAGCATTGAAATCAGACAGCACTGAAGAGGGTGCAGCTGCAGGAG<br>TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu  | 1800<br>600 |
| CTGTCGGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCGCCCCTGCTGACGTCCAGA<br>LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuThrSerArg     | 1860<br>620 |
| CTCCGCTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG<br>LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal  | 1920<br>640 |
| GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA<br>GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla | 1980<br>660 |
| CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGCCCGCCTCTGGCGCCTCTGTG<br>LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal        | 2040<br>680 |
| CTGGGCCTGGACGATATCCACAGGGCTGGCGCACCTCGTGTGCGTGTGCGGGCCAG<br>LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln     | 2100<br>700 |
| GACCCGCCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC<br>AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle  | 2160<br>720 |
| CCCCAGGACAGGCTCACGGAGGTATGCCAGCATCACAAACCCCAGAACACGTACTGC<br>ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys    | 2220<br>740 |
| GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG<br>ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgGlyAlaPheLys  | 2280<br>760 |

Fig. 1C



|  |              |
|--|--------------|
| AGCCACGTCTCACCTTGACAGACCTCCAGCCGTACATGCGACAGTCGTGGCTCACCTG<br>SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu   | 2340<br>780  |
| CAGGAGACCAGCCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG<br>GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu    | 2400<br>800  |
| GCCAGCAGTGGCCTCTCGACGTCTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC<br>AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle   | 2460<br>820  |
| AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG<br>ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu | 2520<br>840  |
| CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCCGGGATTGGCGGGGAC<br>LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp   | 2580<br>860  |
| GGGCTGCTCCTGCGTTGGATGATTCTTGGTGCACACCTCACCTCACCCACGCG<br>GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla        | 2640<br>880  |
| AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTG<br>LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu  | 2700<br>900  |
| CGGAAGACAGTGGTGAACCTCCCTGTAGAACAGCAGGCCCTGGTGGCACGGCTTTGTT<br>ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal   | 2760<br>920  |
| CAGATGCCGCCACGGCCTATTCCCTGGTGCAGCCTGCTGGATACCCGGACCCCTG<br>GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuAspThrArgThrLeu         | 2820<br>940  |
| GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTC<br>GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe   | 2880<br>960  |
| AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGGCTG<br>AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu     | 2940<br>980  |
| AAGTGTACAGCCTGTTCTGGATTGAGGTGAAACAGCCTCCAGACGGTGTGCACCAAC<br>LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn    | 3000<br>1000 |
| ATCTACAAGATCCTCCTGCTGCAGCGTACAGGTTCACCGCATGTGTGCTGCAGCTCCCA<br>IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro     | 3060<br>1020 |

Fig. 1D



|   |  |
|---|--|
| TTTCATCAGCAAGTTGGAAGAACCCACATTTCTGCGCGTACATCTGACACGGCC<br>PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla  | 3120<br>1040   |
| TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC<br>SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly  | 3180<br>1060   |
| GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC<br>AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu   | 3240<br>1080   |
| AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG<br>LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln   | 3300<br>1100   |
| ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC<br>ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn  | 3360<br>1120   |
| CCGGCACTGCCCTCAGACTCAAGACCATCCTGGACTgtatggccacccgcccacagccag<br>ProAlaLeuProSerAspPheLysThrIleLeuAsp  | 3420<br>1132   |
| Gccgagagcagacaccagcagccctgtcacgccggctctacgtcccaaggagggaggg<br>Cggcccacacccaggccccgccccgtggaggtctgaggcctgagtgatgtttggccgag<br>gcctgcattgtccggctgaaggctgagtgccggctgaggcctgagcgtgtccagccaa<br>gggctgagtgccaggcacacccgtccgtttcactccccacaggctggcgctcggtcca<br>ccccaggccagctttccctcaccaggagccccgttccactccccacatggaaatgg<br>catccccagattcgccattgttcccccctcgccctgcccctccatggaaatgg<br>catccagggtggagaccctgagaaggaccctggagctctggaaattggagtgacca<br>gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgg<br>ggggggaggtgctgtggagtaaaatactgaatatatgagttttcagtttggaaaa<br>aaaa | 3480<br>3540<br>3600<br>3660<br>3720<br>3780<br>3840<br>3900<br>3960<br>3964 |

Fig. 1E



Euplotes 1 -----MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIWKVIRCR--NQSQSHYKDLEDIK  
 HT1 1 RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDAR-PPPAAPSFRQVSCLKEVARVLRQLCERGAKNVLAFGFALLDGA  
 EST2 1 -----MKILFEFIQDKLDID--L0TNSTYKENLKCG

Euplotes 56 IFAQTNIVATPRDYNEEDFKVIARK-----EVFSTGLMIELIDKCLVELLSSSDVSDRQKLCQCFGFOLKSGNQ-LAK  
 HT1 80 RGGPPEAFTTSVRSYLPNTVDALRGSGAWGLLRRVGDVLVHLLARCALFVLVAPSCAY--QVCGPPLYQLGAAATQA  
 EST2 30 HFNGLDEILTT-CFALPNSRKIALP-----CLPGDLSHKAVIDHCIYLLTGELYNN--VLTFGYKIARNEDVNN

Euplotes 126 THLLTALSTQKQYFFQDEWNQVRAMIGNEFRHLYTKYLIFQRTSEGTLVQFCGNVFDHLKVNDKFDKKQKGGAADMNE  
 HT1 157 RPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG  
 EST2 97 SLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQ-FFTQIVGNRCNEPHLPPKWVQRSSSS-----

Euplotes 206 PRCCSTCKYNVKNEKDHFLLNI-----NVPNWNMKSRTTRIFYCTHFNRRNQFF  
 HT1 237 PSDRGFCVVSARPAEATSLLEGALSGTRHSHPSVGRQHHAGPPSTSRRPPRWDTCPVVAYETKHFYSSGDK--EQLR  
 EST2 169 -----SATAAQIKQLTEPVTN-----KQFLHKLNIN-SSSFF

Euplotes 255 KKHEFVSNKNNISAM-DRAQTIFTNI-----FRFNIRKKLKDKVIEKIAYMLEVKDFNFNYYLTKSCPLPENWRE  
 HT1 315 PSFLLSSLRPSLTGARRLVTIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTP  
 EST2 200 PYSKILPSSSSIKKLTDLREAIFP-----TNLVKIPQRLKVRINLTLOKLLKRHKRLNYVSILNSICPPLGET--  
 Telomerase domain

Euplotes 326 RK----QKIENLINKTREEKS--KYYEELFSYTTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKKYVELNKHE  
 HT1 394 AAGVCAREKPQGSVAAPEEEEDTPRRLVQLRQHSSPQVYGFVRACLRRLVPPGLWGSRHNERFLRNTKKFISLGKHA  
 EST2 268 -----VLDLSHLSRQ-----SPKERVLKFIIVILQKLLPQEMFGSKKNKGKIKNLNLLSLPLNG

Euplotes 398 LIHKNLLEKINTREISWMQVET-SAKHFYYFDHENIYVWKLLRWIFEDLVVSLIRCCFYVTEQQKSYSKTYYRKNIW  
 HT1 474 KLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHRLEEILAKFLHWLMSVYVVELRSFFYVTETTFQKNRLFFYRKSVW  
 EST2 324 YLPFDSSLKKLRLKDFRWLFISD-IWFTKHNFENLN-QLAICFISWLFRQLIPKIIQTFYYCTEIS-STVTIVYFRHDTW

Motif 1 Motif 2

Euplotes 477 DVIMKMSIADLKK-ETLAEVQEKEVEEKKSL-GFAPGKRLIPKKTT--FRPIMTFNKKIVNSDRK--TTKLTNTKLL  
 HT1 554 SKL0SIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG--LRPIVNMDYVVGARTFRREKRAERLTSRK  
 EST2 401 NKLITPFIVEYFK-TYLVENNCRNHSYTLS-NFNHSKMRRIIPKKSNNEFRIIAIPCRGADEEEFT--IYKENHKNAIQ

Fig. 2A



Motif A

Euplates 551 NSHMLMLKTLKN-RMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLSS  
 HT1 632 ALFSVLNYERARR--PGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVVDVTGAYDTIPQDRLTEVIASIICKPQN  
 EST2 477 PTOKILEYLRNKRPTSFTKISPTQIADRIKEFKQRLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDALKNEN

Euplates 629 DFWIMTAQILKRKNNIVIDSKNFRKEMKDYFRQFQKIALEGQYPTLFSVLENEQNDLNAKTLIVEAK-CRNYFKKD  
 HT1 710 TYCVRRYAVVQKAAGHGVRFKAFKSHVS-----TLTDLQPYMRQFVAHLQETSPRLDAVVIQSSLNEASSG  
 EST2 556 GFFVRSQYFFN-TNTGVLKLFNVVN-----A--SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIFKT-

Motif B Motif C

Euplates 708 NLLOPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT  
 HT1 777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIPQGSILSTLLCSLCYQDMEN---KLFAGIRRD-----GLLLRLVDDFLLV  
 EST2 616 --ALWVEDKCYIR-----EDGLFQGSSLSAPIVDLVYDDLEFYSEFKASPSQD-----TLILKLAADFLIIS

Motif D Motif E

Euplates 788 TQENNAVLFIEKLINVSRENGKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIQDYCDWIGISIDMKTALMPNINLR  
 HT1 847 PHLTHAKTFLRTLVRGVPEYGCVVNLRKTVNFPVEDEALGG-TAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYAR--  
 EST2 677 TDQQ-QVINIKKLAMG---GFQKYNAKANRDKILAVS-----SQSDDDTVIQFCAMHIFVKELEVWKHSSTMN--

Euplates 868 EGILCTLNLMQTKKASMLKLLKSFLMNNITHYFRKTITTEDFANK7LNKLFISGGYKYMQCAKEY--KDHFKKNLAM  
 HT1 924 TSIRASLTFNRGFKAGRNMRRKLFGVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLPFHQQVWKNP  
 EST2 741 -----NFHIRSKSS---KGIFRSLIALNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINV  
 TQ

Euplates 946 SSMIDLEVKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIEIFSTKKYIFNRVCMILKAKEAKLKSDOCQS  
 HT1 1004 FLRVIISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLP  
 EST2 808 NMQFHSFLQRIIEMTVSG---CPITKCDPLIEYEV--FTI--LNGFLESLSNTSKF-KDNIILLRKEIQHLOAYIYI

Euplates 1026 LIQYDA-----  
 HT1 1083 TLTALEAAANPALPSDFKTILD  
 EST2 879 YIHIVN-----

Fig. 2B

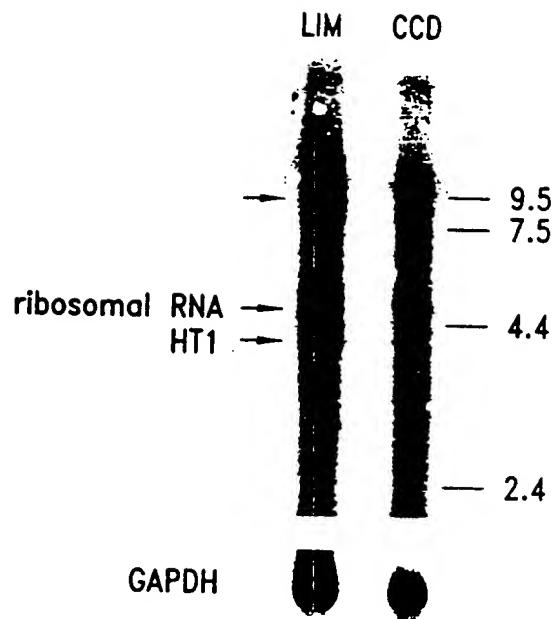


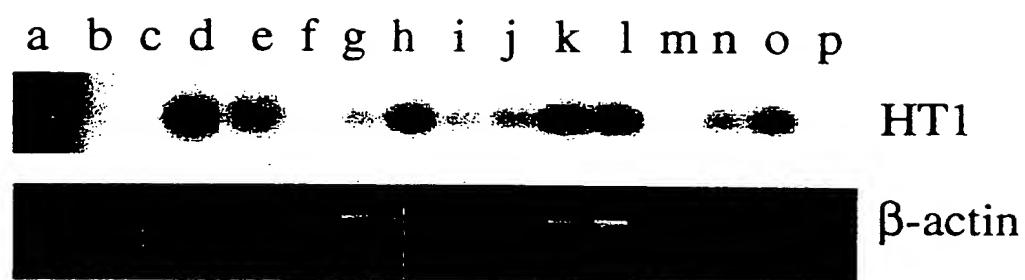
Fig. 3



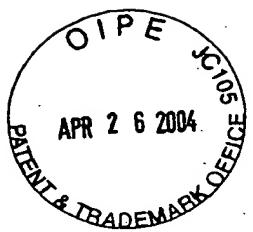
| Plasmid | Human blood |   |   |   | LIM1215 |   |   |   |   |   |   |   |
|---------|-------------|---|---|---|---------|---|---|---|---|---|---|---|
| 10      | 5           | 1 | H | E | P       | X | B | H | E | P | X | B |



*Fig. 4*



*Fig. 5*



*Fig. 6*

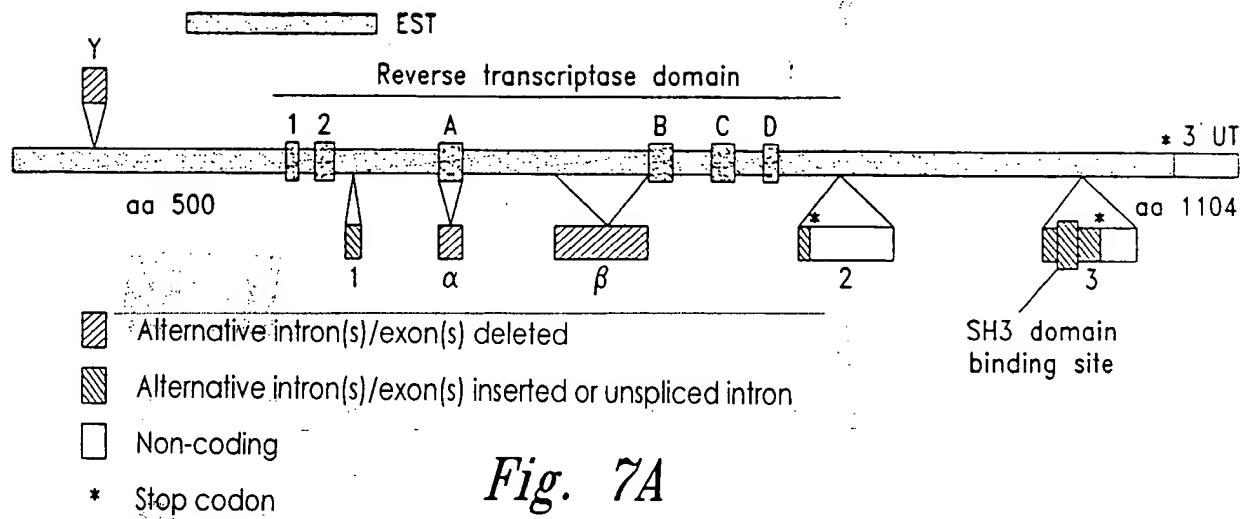


Fig. 7A

| Variants:             | 1  | $\alpha$ | $\beta$ | 2  | 3     |
|-----------------------|----|----------|---------|----|-------|
| RT-PCR product        | NO | +        | +       | NO | + & - |
| PCR from LIM1215 lib. | -  | +        | -       | +  | NO    |
| RT-PCR product        | NO | -        | +       | NO | +     |
| 53.2 cDNA             | -  | -        | -       | -  | NO    |

Fig. 7B



|   |  |                                   |
|---|--|-----------------------------------|
|   | 222  | 223                               |
| Y | 5'-CCAGGTG ggcctc  | gcaggtg TCCTGCC-3'                |
|   | 1950   | 1952                              |
| 1 | 5'-AAAGAGG GTGGCTG.....                                    | AACAGAA GCCGAGC-3'                |
|   | 2130   | 2167                              |
| a | 5'-TGTCAAG gtggatg.....                                    | cccccag GACAGGC-3'                |
|   | 2286   | 2468                              |
| b | 5'-GAGCCAC gtctcta.....                                    | ggggcaa GTCCTAC-3'                |
|   | 2843   | 2844                              |
| 2 | 5'-ACTCCAG GTGAGCG.....                                    | XXXXXXX CTATGCC-3'                |
|   | 3157   |                                   |
| 3 | 5'-AACGCAG CCGAAGAAAACATTCTGCGTGA                          | CCTGCCGTGCTGGGTCGGGACAGCCAGAGATGG |
|   | T A A E E N I L V V T P A V L G S G Q P E M E              |                                   |
|   | AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTCCGGTGTCTCTGGGAGGGGAGTTG |                                   |
|   | P P R R P S G V G S F P V S P G R G V G                    |                                   |
|   | 3158   |                                   |
|   | GGCTGGGCCTGTGACTCCTCAGCCTCTGTTCCCCAG GGATGTC-3'            |                                   |
|   | L G L *  |                                   |

Fig. 7C



a b c d e f g h i j k l



- 430 bp  
- 400  
- 250  
- 220

*Fig. 8*



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTTGCTGCCAGGGCCAGGGTTGGCTGTTCCGGCGCAGAGCACCGTCTGGTGAAGGAGATCCTGGCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTCGAGCTGCTCAGGCTTTCTTATGTCACGGAGACACGCTTTCAAAGAACAGGCTTTCTACCGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
  
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGCGGAAGCAGGGTCAGGCAGCATCGGAAGGCCAGGCCGCTGCTGACGTCAGACTCCGCTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
  
CGGGCTGGCCGATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTAGCGTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
  
GCGGCCGCGCGCCCCGGCTCTGGCGCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCAGCTTGCTGCGTGCAGGGCCAGGACCCGGCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
  
TGTCAAGGTTGGATGTGACGGCGCGTACGACACCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
  
GAAGGCCGCCATGGCACGTCGCAAGGCTTCAAGAGCCAC  
K A A H G H V R K A F K S H

GTCCCTACGTCCAGTG  
V L R P V

CCAGGGGATCCCGAGGGCTCCATCCCTCCACGGCTGCTGAGGCTGTGCTACGGGACATGGAGAACAGCTGTTCCGGGGATTCCGGGGACGGCTGCTCCCTGGTTGGTGGAP  
G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G  
  
TGATTTCTTGTGGTACACCTCACCTCACCCACGC  
\* GAAAACCTCCTCAGGACCCGGTCCGAGGTGTCCCTGAGTATGGCTCCGTGGTAACCTGGGAAGACAGTGGTGAACCTGGCC

Fig. 11AA



Reference protein (ver. 2)

|  |     |
|--|-----|
| ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG     | 60  |
| MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu     | 20  |
| <br>   |     |
| GTGCTGCCGCTGGCCACGTTCGTGCAGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG     | 120 |
| ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln     | 40  |
| <br>   |     |
| CGCGGGGACCCGGCGGCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG      | 180 |
| ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp     | 60  |
| <br>   |     |
| GACGCACGGCCGCCCGCCGCCAGGTG                                       |     |
| AspAlaArgProProProAlaAlaProSerPheArgGlnVal                       |     |
| <br>   |     |
| GGCCTCCCCGGGGTCGGCGTCCGGCTGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAG |     |
| G L P G V G V R L G L R A A G G N Q R H A E                      |     |
| A S P G S A S G W G * G R P G G T S D M R R                      |     |
| P P R G R R P A G V E G G R G E P A T C G E                      |     |
| <br>   |     |
| AGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG                           |     |
| S S A G D S G R F P R R  |     |
| A A Q A T Q G A S P A G  |     |
| Q R R R L R A L P P Q V  |     |
| <br>   |     |
| TCCTGCCTGAAGGAGCTG   | 240 |
| SerCysLeuLysGluLeu   | 80  |
| <br>   |     |
| GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTCGC        | 300 |
| ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly     | 100 |
| <br>   |     |
| TTCGCGCTGGACGGGCCGCGGGGGCCCCGAGGCCTTCACCACCAAGCGTGC              | 360 |
| PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg     | 120 |
| <br>   |     |
| AGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGCGTGGGGCTGCTG        | 420 |
| SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu     | 140 |
| <br>   |     |
| TTGCGCCGCGTGGCGACGACGTGCTGGTCACCTGCTGGCACGCTGCGCGCTTTGTG         | 480 |
| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal     | 160 |
| <br>   |     |
| CTGGTGGCTCCAGCTGCGCCTACCAGGTGTGGGGCGCCGCTGTACAGCTCGCGCT          | 540 |
| LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla     | 180 |
| <br>   |     |
| GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCGAAGGCGTCTGGATGCGAA         | 600 |
| AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu        | 200 |

Fig. 11AB



|  |      |
|--|------|
| CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGCCTGCCAGCCCCGGT    | 660  |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 220  |
| GCGAGGAGGCCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT     | 720  |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 240  |
| GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGCTGGGCCACCCGGC        | 780  |
| GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 260  |
| AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA   | 840  |
| ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 280  |
| GAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCCACCCATCCGTGGC         | 900  |
| GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 300  |
| CGCCAGCACACGCCGGCCCCCATCCACATCGCGCCACCACGTCCCTGGGACACGCC     | 960  |
| ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 320  |
| TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGGAGCAG  | 1020 |
| CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 340  |
| CTGCGGCCCTCTTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC        | 1080 |
| LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 360  |
| GTGGAGACCATTTCTGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCC      | 1140 |
| ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 380  |
| CGCCTGCCCAAGCGCTACTGGCAAATCGGCCCTGTTCTGGAGCTGCTGGAAACCAC     | 1200 |
| ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 400  |
| GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCAGGCCGCTGCGAGCTGCGGTCA       | 1260 |
| AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 420  |
| CCAGCAGCCGGTGTCTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCGAGGAG     | 1320 |
| ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 440  |
| GAGGACACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG   | 1380 |
| GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln | 460  |
| GTGTACGGCTTCGTGGGCCCTGCCTGCGCCGGCTGGTCCCCAGGGCTCTGGGGCTCC    | 1440 |
| ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer | 480  |
| AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCAT   | 1500 |
| ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 500  |
| GCCAAGCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTGGCTG    | 1560 |
| AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 520  |

Fig. 11AC



|  |             |
|--|-------------|
| CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTCGTGAGGAGATC<br>ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle  | 1620<br>540 |
| CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC<br>LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe       | 1680<br>560 |
| TTTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTC<br>PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal      | 1740<br>580 |
| TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGCAGCTGCGGGAG<br>TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu  | 1800<br>600 |
| CTGTCGGAAGCAGAGGTCAAGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCCAGA<br>LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg   | 1860<br>620 |
| CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG<br>LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal | 1920<br>640 |
| GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA<br>GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla | 1980<br>660 |
| CTGTCAGCGTGCTCAACTACGAGCGGGCGCGCCCGCCCTGGCGCCTCTGTG<br>LeuPheSerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerVal             | 2040<br>680 |
| CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGTGCGTGTGCGGCCAG<br>LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln     | 2100<br>700 |
| GACCCGCCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC<br>AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle     | 2160<br>720 |
| CCCCAGGACAGGCTCACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGC<br>ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys   | 2220<br>740 |
| GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGCACGTCCGCAAGGCCTCAAG<br>ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys    | 2280<br>760 |
| AGCCACGTCTCACCTGACAGACCTCCAGCGTACATGCGACAGTTCGTGGCTCACCTG<br>SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu    | 2340<br>780 |
| CAGGAGACCAGCCCCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG<br>GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu      | 2400<br>800 |
| GCCAGCAGTGGCCTTCTCGACGTCTCCTACGCTTACATGTGCCACCACGCCGTGCGCATC<br>AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle | 2460<br>820 |
| AGGGGCAAGTCCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCATCCTCCACGCTG<br>ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu   | 2520<br>840 |

Fig. 11AD



|  |      |
|--|------|
| CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCGGGGATTGGCGGGAC      | 2580 |
| LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp   | 860  |
| GGGCTGCTCCTGCGTTGGATGATTCTTGGTACACCTCACCTCACCCACGCG            | 2640 |
| GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla   | 880  |
| AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTG    | 2700 |
| LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu   | 900  |
| CGGAAGACAGTGGTGAACCTCCCTGAGAACAGCAGGGCCCTGGGTGGCACGGCTTTGTT    | 2760 |
| ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal   | 920  |
| CAGATGCCGGCCCACGGCTATTCCCTGGTGCAGCCTGCTGGATACCCGGACCCCTG       | 2820 |
| GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu   | 940  |
| GAGGTGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCACCTC     | 2880 |
| GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe   | 960  |
| AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACACTTTGGGTCTGGCGCTG     | 2940 |
| AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu   | 980  |
| AAGTGTACAGCCTGTTCTGGATTGCAAGGTGAAACAGCAGGCTCCAGACGGTGTGCACCAAC | 3000 |
| LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn   | 1000 |
| ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCA     | 3060 |
| IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro      | 1020 |
| TTTCATCAGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCATCTGACACGGCC         | 3120 |
| PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla   | 1040 |
| TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC    | 3180 |
| SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly   | 1060 |
| GCCGCCGGCCCTGCCCCTCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC      | 3240 |
| AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu   | 1080 |
| AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG     | 3300 |
| LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln   | 1100 |
| ACGCAGCTGAGTCGGAAGCTCCGGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC      | 3360 |
| ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn      | 1120 |
| CCGGCACTGCCCTCAGACTCAAGACCACCTGAC                              | 3420 |
| ProAlaLeuProSerAspPheLysThrIleLeuAsp                           | 1132 |



### Truncated protein 3 (ver. 2)

ATGCCGCGCCTCCCCCTGCCGAGCGCTGCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTC  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGGCCCTGGGGCCCCAGGGCTGGCGCTGGTCACCGCGGGGACCGCGCTTCCGCCGCTGCTGGCCAGTGCCTGGTGTGCCCTGGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
GGCCTCCCGGGTCCGGCTGGGTTGAGGGCGCCGGGGAACCGCAGCATGCCAGAGCAGCAGCCAGGCACTCAGGGCCTCCCCCAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
CCCTCTCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCAGGCCGCGGAAGAACGTGCTGGCCCTGCCCTGCCCTGGACGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTGGCAGCTACCTGCCAACACGCTGACCGACGCAGTGCAGGGAGCCGGCGTGGGGCTGCTGCCCTGCCCTGGGACGGACG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTACCTGCTGGCACGCTGGCGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGCTGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGGCCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGGACCCGAAGGCCTGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGCTCCCTGGCCTGCCAGCCCCGGTGCAGGGAGGCCGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCCTGCCAACAGGGCCAGGCCTGGCGCTGCCCTGAGCGAGCGAGCCGGTGGCAGGGCTGGCCACCCGGCAGGACCGCTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTTGCTCACCTGCCAGACCCGCCAACAGAGCCACCTCTTGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTGGCCGCCACACGCCGGCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGCGCCACCGCTGGACACGCCCTGGTACGCCAGACAGCTCCCTACTCCACAGGAGACCAAGCCTCTACTCCACAGGAGACCTGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGAACATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTCAGTGCCTACGGGGTCTCTCAAGACGACTGCCCTGCCAGCTGCCAGCCAGGCCGTCTGTGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAACCCAGGGCTGTGGCGCCCCAGGCCTCTGGGCTCCAGGCACAAACGAACGCCCTGCCAGGTGACGGCTTCCGCCAGCACAGCAGCCCTGGCAGGTGACGGCTTCCGTGCC  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCGCCCTGGTGGCCCCAGGCCTCTGGGCTCCAGGCACAAACGAACGCCCTGCCAGGAACACCAAGAAGTCATCTCCCTGGGAAAGCATGCCAAGCTCGCTGCCAGGAGC  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L O E L

*Fig. 11AF*



GACGTGGAAGATGAGCGTGGGGACTGCGCTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTTCCGGCCAGAGCACCGCTCGGTGAGGAGATCTGGCAAGTTCTGCACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTGTCAGCTGCTCAGGTCTTCTTTATGTCACGGAGACCACTTCAAAAGAACAGGCTTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
  
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCAGGAGAGGTAGGCAGCATCGGAAGGCCAGGCCCTGCTGACGTCAGACTCCGCTCATCCCCAAGCCTGA  
I R O H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
  
CGGGCTGGGCCATTGTGAACATGGACTACCTCGTGGAGCCAGAACGTTCCAGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTAAGGCAGTGTAGCTGCTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
  
GCGGGCGGGCGCCCGGCCCTCTGGGCGCTCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGACCTCGTGTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
  
TGTCAAGGTGGATGTGACGGCGCGTACGACACCATCCCCAGGACAGGCTACGGAGGTACGCCAGCATCATCAAACCCAGAACACGTAAGCTGCGTGCCTGAGCTGACT  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
  
GAAGGCCGCCATGGCACGTCGCAGGCCCTCAAGAGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCCAGCAGTCAGTTGCTGGCTACCTGCAAGGAGACCAGCCGCTGAGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
  
TGCGCTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTGACGCTTCTACGCTTATGTGCCACACGCCGTGCATCAGGGCAAGTCCTACGTCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
  
CCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGACGCCCTGCTACGGGACATGGAGAACAGCTGTTGCGGGATTGCGCCGACGGCTGCTCTGCGTTGG  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
  
TGATTTCTTGTGGTACACCTCACCTCACCCACCGAAAACCTTCTCAGGACCTGGTCCAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGCGGAAGACAGTGGTAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
  
TGAGAAGACGAGGCCCTGGGTGGCACGGCTTGTAGATGCCGCCACGCCATTCCCTGGTGCCTGCTGGATAACCCGACCCCTGGAGGTGAGAGCAGACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R  
  
GTGAGCGCACCTGGCGGAAGTGGAGCCGTGCCCCGGCTGGGCAAGGTGCTGCTGAGGCCCTTGCGTCCACCTCTGCTTCCGTGTGGCAGGCAGTGCACATCCAAAGGGTCA  
\*  
  
TGCCACAGGGTGCCCTCTCCATCTGGGCTGAGCACAAATGCATTTCTGTGGAGTGAGGTGCTCACACGGAGCAGTTCTGTGCTATTTGGTAA.....

Fig. 11AG



Altered C-terminus protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGTCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCACGTTGTC  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGCCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCAGCTGGCCAGTGCCTGGTGTGCCCTGGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
GGCCTCCCGGGCTGGCGCTGGGTGAGGGCGCCGGGGAAACAGCGACATGCCAGAGCAGCCAGCGACTCAGGGCGCTCCCCCGAGGT  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
|.  
CCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGCTGTGCGAGCGCGCGAAGAACGTGCTGGCTTCGGCTCGCCTGCTGGACGGGCCG  
P S F R Q V S C L K E L V A R V L O R L C E R G A K N V L A F G F A L L D G A R  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACAGGTGACCGACGCAC TGCGGGGAGCGGGCTGCTGCGCCGCTGGGACGACG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
GCTGGTTACCTGCTGGCACGCTGGCGCTTTGTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGGCCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
ACACGCTAGGGACCCGAAGGCCCTGGATGCAACGGCCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGCCTGCCAGCCCCGGTGCAGAGGCCGGCAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
CAGCCGAAGTGTGCCCTGCCAACAGGCCAGGCGTGGCGCTGCCCTGAGCCAGCGAGGCCGGTGGCAGGGCTGGGCCACCCGGCAGGACCGTGGACCGAGTC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
TGGTTCTGTGGTGTACCTGCCAGACCCGCCAACGACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGCCGCGACACCACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
ATCCACATGCCGCCACCGCTCCGGACACGCCCTGGTACGCCAGACCAAGCCTCCCTACTCCAGGCCACAAGGAGCAGCTGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGCGAGCTGCCCTACGGGGTGCCTCAAGACGCACGCCCTGCCAGCTGCCAGGCCAGCGCTGTGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
GGAGAACCCAGGGCTGTGGCGCCCGAGGAGGAGCACAGACCCCGTCCCTGGTGCAGCTGCCAGCACAGCAGCCCTGGCAGGTACGGCTCGCAGGGCT  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
CTGCCGCCCTGGTCCAGGCCCTGGGCTCAGGCACAACGAACGCCCTCCCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAGCTCGCAGGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

*Fig. 11AH*



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GACGCTGGAAAGATGAGCGTGGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTGGCTGTCTGGCCAGAGCACCGTCTGCGTGGAGATCTGGCAAGTTCTGACTGGCT  
TW K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTGTCGAGCTGTCAGGTCTTCTTATGTACGGAGACCACTGGTCAAAAGAACGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG  
M S V Y V V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
  
AATCAGACACCACTGAAGAGGGTGCAGCTGCGGGAGCTGCGGAAGCAGAGGTAGGCAGCATGGGAAGCCAGGCCCTGCTGAGTCCAGACTCCGCTCATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
  
CGGGCTGCGGCCGATTGTAAACATGGACTACGTCGAGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCGAGCGTCACTCGAGGGTGAAGGACTGTCAGCGTCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
  
GCGGGCGCGCCGCCCCGGCTCTGGCGCCCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTCTGCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
  
TGTCAAGGTGGATGTGACGGGCCGACGACACCATCCCCAGGACAGGCTACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTAACGTCGCGTCGGTATGCCGTGGTCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
  
GAAGGCCGCCATGGGCACGTCGCCAAGGCCCTCAAGAGCCACGTCTACCTTGACAGACCTCCAGCCATGCGACAGTCGCGCTCACCTGCAGGAGACCAAGCCCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
  
TGCCGTCGTATCGAGCAGAGCTCCCTGAATGAGGCCAGCACTGGCTCTTGACGCTTCCCTACGCTCATGCGACCCCTGCCATCAGGGCAAGTCTACGTCAGT  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V O C  
  
CCAGGGGATCCGCAGGGCTCATCTCTCCACGCTGCTCTGACGCTGCTACGGCGACATGGAGAACAGCTGTTGGGGATTGGCGGGACGGCTCTCCGCTTGG  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
  
TGATTTCTTGGTGAACCTCACCTCACCCACGCCAAACCTTCTCAGGACCTGGTCCAGGGTGTCCCTGAGTATGGCTGCGTGGTAACCTGCGGAAGAACAGTGGTGAACCTCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
  
TGTAGAAGACGAGGCCCTGGTGGCACGGCTTGTGACATGCCGCCACGGCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGACCCCTGGAGGTGCAAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
  
CTATGCCGGACCTCCATCAGAGCCAGTCACCTCACCGCGCTCAAGGCTGGAGGAACATGCGTCGAAACTCTTGGGTCTTGCGCTGAAGTGTACAGCTGTTCTGG  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
  
TTTGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAAGATCCTCTGCTGAGGCTACAGGTTCAAGCATGTTGCTGAGCTCCATTCTACAGCAAGTTGGAGAA  
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H Q Q V W K N  
  
CCCCACATTTCTGCGGTATCTGACACGCCCTCCCTCTGCTACTCCATCTGAAAGCAAGAACGAGGGATGTCGTTGGGGCAAGGGCGCCGCCCTGCGCTCCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A E  
  
CCGAAGAAAACATTCTGCGTGAACCTGGCTGGCTGACTCTGCGTGGCTGGTC  
E E N I L V V T P A V L G S  
  
GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTGGGTGGCAGCTTCCGGTGTCTGGAGGGAGTTGGCTGGCCCTGACTCCTCAGCCTGTTCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

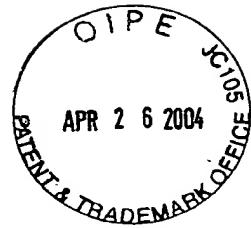
Fig. 11AI



### Protein that lacks motif A (ver. 2)

ATGCCGCGCGTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACCGCAGGTGCTGCCCTGGCACGTTGCGT  
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
 CGGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGGCACGCCACGGCCGCCCCCGCCG  
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
 GGCCTCCCGGGTCGGCGTCCGGCTGGGTGAGGGCGCCGGGGAAACAGCAGCATGCCAGCGAGAGCAGCGCAGGCAGCTCAGGGCGCTTCCCGCAGGTG  
 G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
 A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
 CCCCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCGAGTGCAGAGGTGTCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTGCTGGACGGGCCCC  
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
 CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCACGCACTGCCAGGGAGCGGGCGTGGGGCTGCTGCTGCCCGCGTGGCGACGAGT  
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
 GCTGGTTCACCTGCTGGCACGCTGCCCTTTGTGCTGGTGGCTCCAGCTGCCCTACCGGTGTCGGGGCCGCGCTGTACCAAGCTGGCGCTGCCACTCAGGCCGGCCCCGCC  
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
 ACACGCTAGTGGACCCGAAGGCGTCTGGGATGCGAACGGCCTGGAAACCATAGCGTCAGGGAGGCCGGTCCCTGGGCTGCCAGCCCGGGTGCAGGGAGGCCGGGGCAGTGC  
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
 CAGCCGAAGTCTGCCGTGCCAAGAGGCCAGCGTGGCGCTGCCCTGAGCCGAGCGCACGCCGTTGGCAGGGCTGGCCACCCGGCAGGACGCGTGGACCGACTGACCG  
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
 TGGTTCTGTGTTGTCACCTGCCAGACCCGCCAGAGAAGCCACCTCTTGAGGGTGCCTCTGGCACGCCACTCCACCCATCGTGGCCAGCACCACGCCGGCCCC  
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
 ATCCACATCGGGCCACACGCTCCCTGGACACGCCCTGCCCCGGTACGCCAGACCAAGCAGCTCTACTCTCAGGCAGCAAGGAGCAGCTGCCCTCTCTACTCAG  
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S  
  
 CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTGAGGACCATCTTCTGGGATGCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCTGCCAGGCCACTGGCA  
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
 AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGCGCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCAGCTGCCAGCCAGGCCAGGCCAG  
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
 GGAGAAGCCCAAGGGCTGTGGCGCCCCAGGCCTCTGGGCTCCAGGCACAACGAACGCCCTGCCAGGAGGACACAGACCCCGTCGCTGGTACGGCTGGAGGAGCTG  
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
 CCTGCGCCGCTGGTGGCCCTGGGCTCCAGGCACAACGAACGCCCTGCCAGGAGGACACAGACCCCGTCGCTGGTACGGCTGGAGGAGCTGCCAGCTCGCTGCCAG  
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

*Fig. 11AJ*



GACGTGAAAGATGAGCTGGGGACTGCCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGCCAGACCCGCTGGTGGAGATCTGCCAAGTCCGCACGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGACGTCGAGCTGCTCAGGCTTTATGTACGGAGACACGTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTGGACCAAGTTGCAAACCATGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGCGGAAGCAGAGGTAGGCAGCATCGGAAGCCAGGCCGCTGTCAGTCCAGACTCCGTTATCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGCCGCGATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGCTCACCTCGAGGGTAAGGCAGTGTACGCTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
GGGGCGCGCGGCCGCGCTCTGGCGCCCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGACCTCGTGTGCGTGGCCAGGACCCGCCGCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTAACGCTGCGTGCCTGATGCCGTCAGCTGCTGCTAAC  
V K D R L T E V I A S I I K P O N T Y C V R R Y A V V Q  
GAAGGCCCATGGCACGTCGAAGGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCGACAGTGTGGCTACCTGCAGGAGACAGCCGCTGAGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
TGCGTCGTCATGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTCTACGTTCATGTGCCACACGCCGCGCATCAGGGCAAGTCCACGTCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
CCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGAGCCGACATGGAGAACAGCTGTTGGGATTGGCGGACGGCTGCTCTGCCTGGTGG  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
TGATTCTGGTGAACCTCACCTCACCCACGGAAAACCTCTCAGGACCTGGCTGAGGTCTCTGAGTATGGCTGGTGAACCTGGGAAGACAGTGTGAACCTCCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
TGAGAAGACGAGGCCCTGGTGCACGGCTTCTAGATGCCGCCACGGCTATTCCCTGGTGCCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
CTATGCCGACCTCCATCAGAGCCAGTCACCTCAACCGCCCTCAAGGCTGGAGAACATGCGCGAAACTCTTGGGCTTGGCTGAAGTGTACAGCTGTTCTGG  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
TTGCAGGTGAACAGCCTCAGACGGTGTGACCAACATCTACAAGATCCTCTGCTGCAGGGTACAGTTACGCATGTGCTGCAGCTCCATTCTACAGCAAGTTGGAAAGAA  
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H O Q V W K N  
CCCCACATTTCTGCGCTCATCTGACACGGCTCCCTGCTACTCCATCTGAAGCCAAGAACGAGGGATGCGCTGGGGCAAGGGGCCGCGCCCTGCCCCTCGA  
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E  
GGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTCACTACGTCACCTGGGACTCAGGACAGCCAGACGAGCTGAGTCGGAAAGCTCC  
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T O L S R K L P  
GGGAGACGCTGACTGCCCTGGAGGCCAGCCAACCCGGACTGCCCTCAGACTCAAGACCATCTGGACTGATGCCACCCGCCACAGCCAGGCCAGAGCAGACACCAGCC  
G T T L T A L E A A A N P A L P S D F K T I L D

*Fig. 11AK*



CTGTCACGCCGGCTCACGTCCCAGGGAGGGAGGGCGGCCACACCCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGACTGTTGGCCGAGGCCCTGCATGTCGGCTGAAGGCT  
GAGTGTCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACCTGCCCTTCACCTCCCCACAGGCTGGCGCTGGCTCCACCCAGGGCAGCTTCCCTCAC  
CAGGAGCCCGCTTCACTCCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTTACCCCTGCCCTGCCCTTGCCTTCAACCCACCATCCAGGTGGAGACCCCTGAGAA  
GGACCCCTGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCAGGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGAGTAA  
AATACTGAATATGAGTTTCAGTTGA

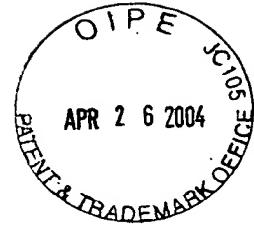
*Fig. 11AL*



Truncated protein that lacks motif A (ver. 2)

ATGCCGCGCCTCCCCCTGCCAGGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCAC  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGCCCTGGGGCCCAGGGCTGGCGCTGGTGCAGCGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGGGACGACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
GGCCCTCCCGGGTGGCGTCCGGCTGGGTGAGGCCAGCAGCGACTAGGGAGAGCAGCGAGGGACTCAGGGCCTCCCCCGAGGT  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
CCCCCTCCGCCAGGTGCTGCCTGAAGAGCTGGTGGCCAGTGCAGAGCTGTGCAGCGCGCGAAGAACGTGCTGGCCTCGGCTCGCCTGCTGGACGGGCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
GGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCAGCAGTGGGGAGCGGGCTGGGCTGCTGCAGCGCGTGGCGACGAGCT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTCACCTGCTGGCACGCTGCGCTCTTGCTGGCTCCAGCTGGCCTACAGGTGCGGGCCCGCTGTACAGCTGGCCTGCCACTCAGGCCGGCCCCCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGGACCCGAAGGCCTGGGATGCAACGGCCCTGGAACCATAGCGTCAAGGAGGCGGGTCCCTGGCCTGCCAGCCCAGGTGCGAGGAGGCGGGCAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCCTGCCAACAGGGCCAGGCCTGGCGCTGCCAGGGTGGCCAGGGTGGCAGGGCTGGGCCACCCGGCAGGAGCGCTGGACCGACTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAAGCCACCTTTGGAGGGTGCCTCTGGCACCGCCTACTCCACCCATCCGTGGCCGCCAGCACACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATGCCGCCAACACGCTCCGGACACGCCCTGGTACGCCAGACCAAGCCTCTGGAGGGTGCCTCTGGCACGGCAGCTGGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGAACACCGCAGTGCCTACGGGTGCTCCCAAGACGCACTGCCGCTGCCAGCTGGTACCCAGCAGCCGTCTGTGCCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGGCCAGGGCTGTGGCGCCCCAGGCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCGGAAAGCATGCCAACCTCGCAG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P H Q V Y G F V R A C  
  
CCTGCCGCCCTGGTGCCTGGGCCAGGCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCGGAAAGCATGCCAACCTCGCAG  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AM



GACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCAGAGCAGCGTCTGCGTGAGGAGATCTGGCAAGTTCTGCACGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGTACGTCGTCAGCTGCTCAGGCTTTCTTTATGTACGGAGACACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AATCAGACAGCACTGAAGAGGGTGCAGCTGGGGAGCTGTCGGAAGCAGAGTCAGGCAGCATCGGAAGCCAGGCCGCTGCTGACGTCCAGACTCCGTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGCGGCCATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGCTCACCTGAGGGTAAGGCAGTGTCAAGCTGCTCAACTACGA  
G L R P I V N M O Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
GCGGGCGGGCGCCCCGGCTCCTGGCGCCCTGTGCTGGGCTGGACGATATCACAGGGCTGGCGCACCTCGTGTGCGTGTGCGGCCAGGACCCGCCGCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTAACGCTGCGTGTGCGTATGCCGTGGCA  
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
GAAGGCCGCCATGGCACGTCGCAAGGCCACGTCACCTGACAGACCTCCAGCGTACATGCGACAGTTGTGGCTACCTGCAGGAGACAGCCGCTGAGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
TGCCGTGTCATCGAGCAGACTCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTCTACGCTTATGTGCCACACGCCGTGCGCATCAGGGCAAGTCACGTCAGTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGCTACGGCAGATGGAGAACAGCTGTTGGGATTGGCGGGACGGCTGCTCTGCGTTGGTGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
TGATTTCTGTTGGTACACCTCACCTCACCCACGGAAAACCTCTCAGGACCTGGTCCAGGTGCTGAGTATGGCTGCGTGGTAACCTGGGAAGACAGTGGTAACCTCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
TGAGAACGAGGCCCTGGTGGCACGGCTTGTAGATGCCGCCACGGCTATTCCCTGGTGGCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R  
GTGAGCGCACCTGGCCGGAAAGTGGAGCCGTGCCCCGGCTGGGAGGTGCTGCAGGGCCCTGGTCCACCTCTGCTTCCGTGCGGGCAGGGACTGCCAATCCCCAAGGGTCAGA  
\*  
TGCCACAGGGTCCCCCTGTCATCTGGGCTGAGCACAAATCCATTTCTGTTGGAGTGAGGGTGCTCACACGGAGCACGTTCTGTGCTATTTGGTAA.....

Fig. 11AN



Lacks motif A and altered C-terminus (ver. 2)

ATGCCGCGCCTCCCCGTGCCAGGCCGTGCCAGCCACTACCGGAGGTGCTGCCCTGGCCACGTC  
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
 CGGCCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGGGACGCACGGCCGCCCCCGCCG  
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
 GGCCTCCCGGGTCCGGTGGGGTGGCCAGCCACGGCAGCTGGCCAGCTGGCCAGCCACGGCAGCTGGCCAGCCACGGCAGCTGGCCAGCCACGGCAGCTGGCCAGGTG  
 G L P G V G V R L G L R A A G G N O R H A E S S A G D S G R F P R R  
 A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
 CCCCTCCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCAGCCGCGCGAAGAACGTGCTGGCCCTCGGCTCGGCTGCTGGACGGGCCCC  
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
 CGGGGGCCCCCGAGGCCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCAGCAGCTGGGGAGGGGGCTGGGGCTGCTGCTGCCCGCGTGGCGACGCT  
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
 GCTGGTCACCTGCTGGCACGCTGCCGCTTTGTGCTGGCTCCAGCTGCCAACACGGTACCGCAGCAGCTGGGGAGGGGGCTGGGGCTGCTGCTGCCACTCAGGCCGGCCCC  
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
 ACACGCTAGTGGACCCGAAGGCAGTGGATGCAACGGCCTGGAAACCATAGCGTACGGAGGGGGCTGGGCTGCCAGCCGGGTGCGAGCCGGGTGCGAGGGGGCAGTGC  
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
 CAGCCGAAGTGTGCCCTGCCAACAGGGCCAGGCAGTGGCTGCCAGCCGGTGGGAGCCGGAGCCGGTGGGAGGGGCTGGGCCACCCGGCAGGAGCCGTGGACCGAGTGC  
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
 TGGTTCTGTGGTGTACCTGCCAGACCCCGAAGAAGCCACCTCTTGGAGGGTGCCTCTGGCACGGCAGCCACTCCACCCATCCGTGGCCAGCACACGCCGGCCCC  
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R O H H A G P P  
  
 ATCCACATGCCGCCACACGCCCTGGACACGCCCTGGTACGCCAGACCAAGCAGCTCCCTACTCCCTAGCGACAAGGAGCAGCTGCCCTCCCTACTCAG  
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
 CTCTCTGAGGCCAGCCTGACTGGCCTGGAGGCTCTGGAGACCATCTTGTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGTACTGGCA  
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
 AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTGCAGTGCCTACGGGTGCTCTCAAGACGACTGCCCTGCCAGCTGCCAGCCAGCAGCCGTGCTGTGCCG  
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
 GGAGAAGCCCCAGGGCTCTGGCGGCCCGAGGAGGAGCACAGACCCCGTCGCTGGAGCAGCACAGCAGCCCTGGCAGGTGACGGCTCGTGCAGGAGCT  
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
 CCTGCGCCGGCTGGTGCCTCCAGGCACAACGAACGCCGCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAGCTGCCAGGAGCT  
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

*Fig. 11AO*



GACGTGGAAGATGAGCGTGGGGACTGGCTGGCTGCGCAGGAGCCAGGGGTGGCTGTTCCGGCCAGAGGCACCGTCTGCGTGAAGGAGATCCTGGCAAGTTCTGCACTGGCT  
THKMSVRDCAWLRRSPGVGCVPAAEHRLREELAKFLHWL  
GATGAGTGTGACGTCGCTGAGCTGCTCAGGCTTTCTTATGTCACGGAGACACGTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLOSI  
AATCAGACAGCACTGAAGAGGGTCAGCTGGGGAGCTGTCGAAGCAGAGGTCAAGCAGCATGGAGCCAGGCCCTGCTGACGTCCAGACTCCGTTCATCCCAAGCCTGA  
IRQHHLKRVQLRELSEAEVROHREARPAALLTSRRLRFIPKPD  
CGGGCTGGGCCATTGTAACATGGACTACGTCGAGGCCAGAACGTTCCGAGAGAAAAGAGGCCAGGGCTCACCTGAGGGTAAGGCAGTGTCAAGCTGCTCAACTACGA  
GLRPIVNMDYVVVGARTFRREKRAERLTSRVKALFSVLNYE  
CGGGGCGGGCGCCCGGCCCTGGGCCCTGTGCTGGCCTGGACGATATCACAGGGCCTGGCACCTTCGCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTACTT  
RARRPGLLGAASVLAGLDDIHRAWRTFVLRVRAQDPPPELYF  
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGGTATGCCGTGCA  
VK DRLTEVIASIIKPQNTYCVRRYAVVQ  
GAAGGCCCCCATGGCACGTCGCCAAGGCCACGTCACCTGACAGACCTCCAGCTACATGCCAGCTGGCTCACCTGAGGGACCCGCTGAGGA  
KA AHGHVRKAFKSHVSTLTDLOPYMRQFVAHLOETSPLRD  
TGCGTCGTCATCGAGCAGAGCTCCCTCCGAAATGAGGCCAGCAGTGGCTCTGACGTTCTACGTTATGTGCCACACGCCGTGCGCATCAGGGCAAGTCTACGTCAGTG  
AVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQC  
CCAGGGATCCCGCAGGGCTCCATCCCTCCACGCTGCTGAGCAGTGGGACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCGTTGGGA  
QGIPQGSILSTLLCSLCYGDMEENKLFAAGIRRDGLLLRLVD  
TGATTCTTGTGGTACACCTCACCTCACCCACGGAAAACCTTCCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGGAGAACAGTGGTAACCTCC  
DFLLVTPTHAKTFLRTLVRGVPEYGCVVNLRKTVVNF  
TGAGAAGACGAGGCCCTGGTGCACGGCTTTGTCAGATGCCGCCACGGCTATTCCCTGGTGCCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
CTATGCCGACCTCCATCAGAGCCAGTCACCTCACCCACGGAAAACCTTCCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTAAGTGTACAGCCTGTTCTGG  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
TTGCAAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAAGATCCTCTGCAAGGCTACGGTACAGGTTACGCACTGCTGCTGAGCTCCATTCA  
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H Q Q V W K N  
CCCCACATTTCTGCGCTCATCTGACACGGCTCCCTGCTACTCCATCTGAAAGCCAAGAACGCAAGGGATGCGCTGGGGCCAAGGGGCCGCCCTGCCCCCGA  
P T F F L R V I S O T A S L C Y S I L K A K N A E  
CCGAAGAAACATTCTGCGTGAETCTGCGTGCTTGGGCT  
E E N I L V V T P A V L G S  
GGGACAGCCAGAGATGGAGCCACCCGAGACCGTGGGTGTGGCAGCTTCCGGTGTCTCTGGAGGGAGTTGGCTGGGCTGTGACTCCTCAGCCTGTTCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

*Fig. 11AP*

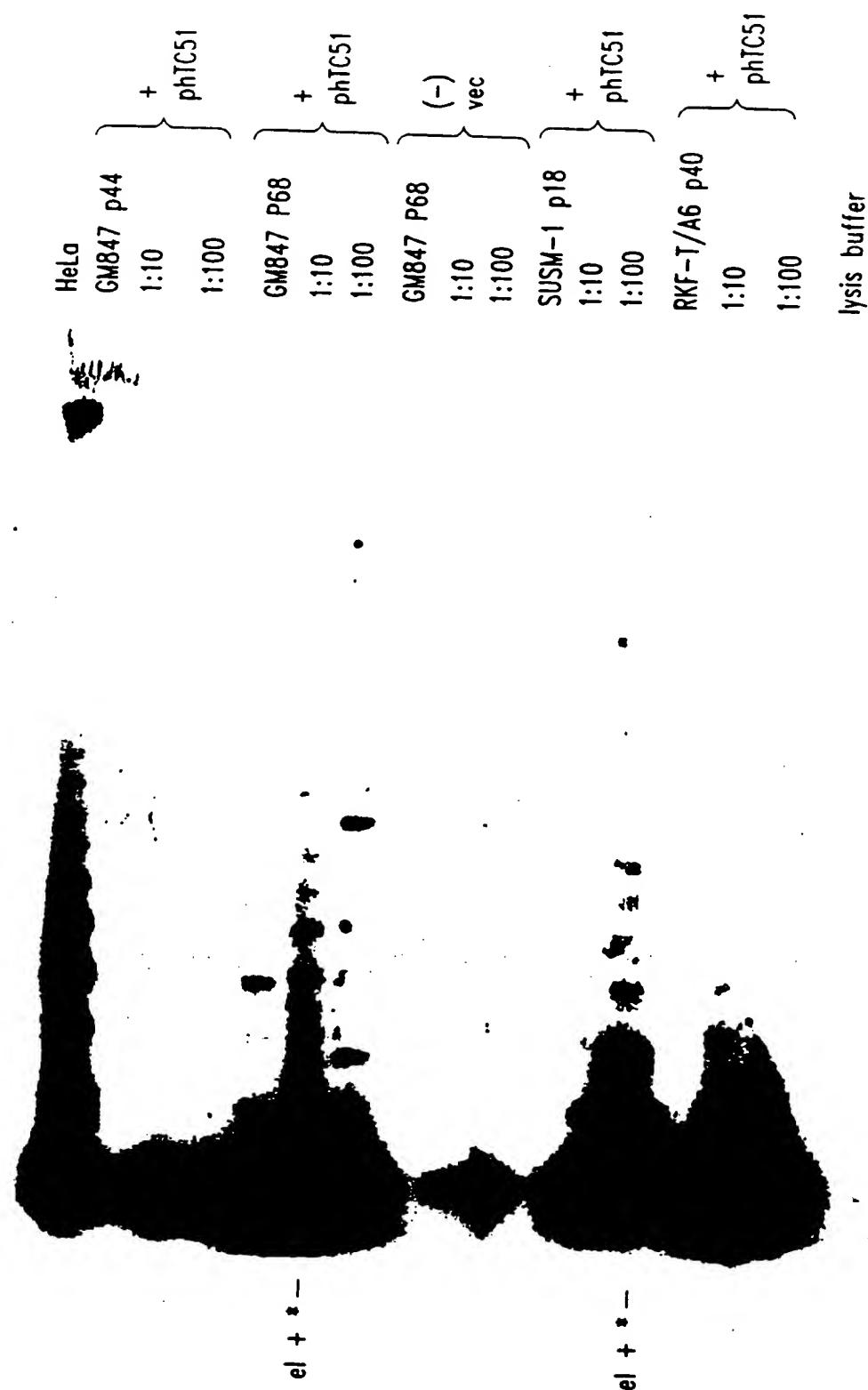


Fig. 12

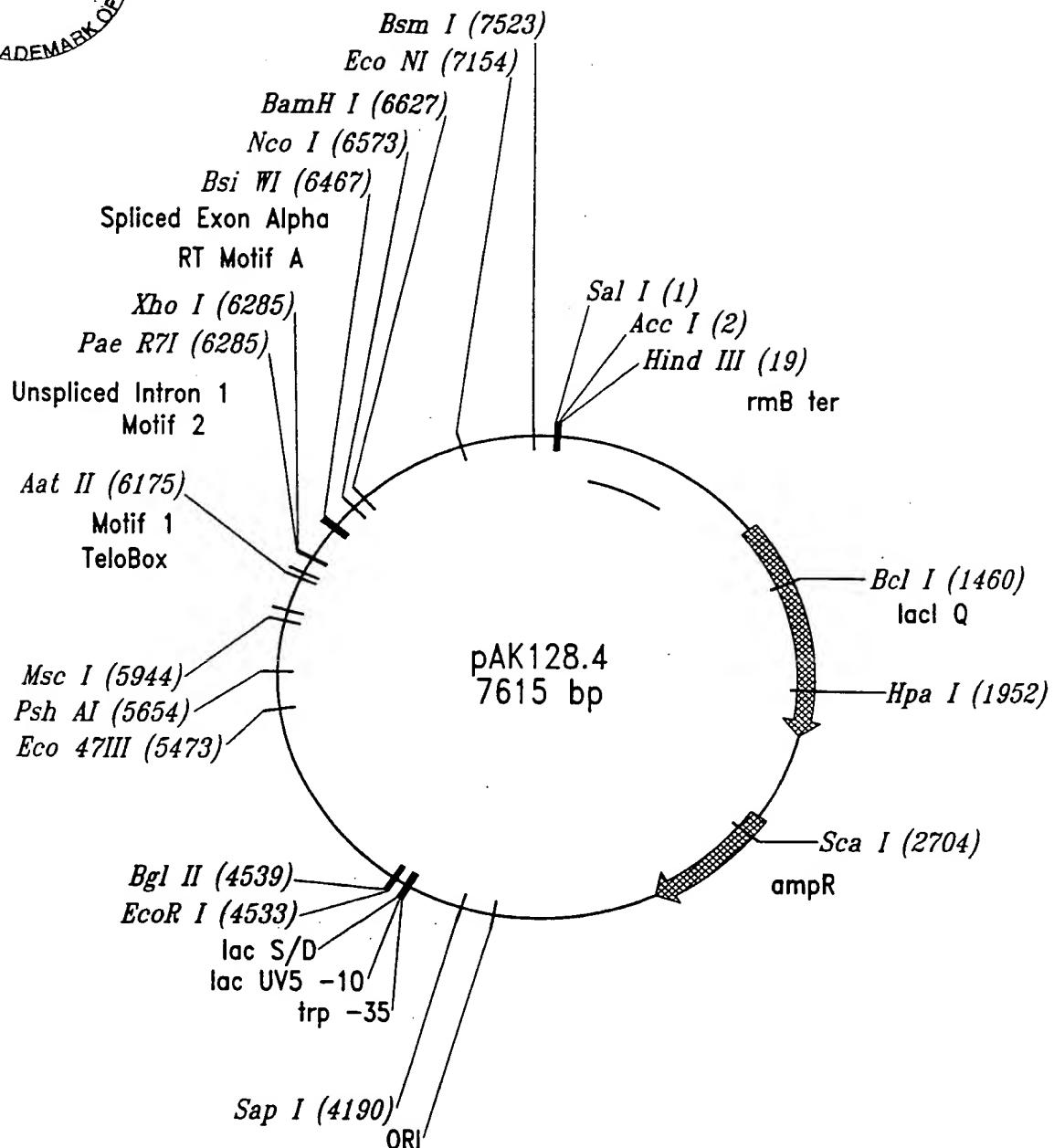


Fig. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular  
DEFINITION Human telomerase clone with exon beta spliced out



1 tcgacctgca ggcatgcaag cttggcactg gccgtcgaaa tacaacgtcg tgactggaa  
61 aaccctggcg ttacccaact taatgcctt gcagcacatc ccccttcgc cagctggcg  
121 aatagcgaag aggccccgac cgatcgccct tcccaacagt tgccgagcct gaatggcgaa  
181 tggccctga tgcgttattt tctccttacg catctgtgcg gtatttcaca ccgcataat  
241 tccctgtttt ggcggatgag agaagattt cagcctgata cagattaaat cagaacgcag  
301 aagggtctg ataaaacaga atttgcctgg cggcagtagc gccgtggcc cacctgaccc  
361 catgccgaac tcagaagtga aacgcgttag cgccgtatgtt agtgtgggt ctccccatgc  
421 gagagttaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct  
481 ttcgttttat ctgttgggg tcggtaacg ctccctgag taggacaat ccgccccggag  
541 cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgcataaaa  
601 ctgcaggca tcaaattaag cagaaggcca tcctgacgga tggcctttt gcgttctac  
661 aaactcttcc tgcgtcata tctacaagcc atccccccac agatacggtt aactagcctc  
721 gttttgtcat caggaaagca gggaaatttat ggtgcactt cagtacaatc tgctctgtat  
781 ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacggcctt  
841 gtctgtccc ggcattccgc tacagacaag ctgtgaccgt ctccgggagc tgcatgtgc  
901 agaggtttc accgtcatca cggaaacgcg cgagacgaaa gggcctcgat atacgcctat  
961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca  
1021 ccatcgaatg gtgaaaacc tttcggta tggcatgata ggcggccggaa gagagtcaat  
1081 tcagggtggtaatgtgaaa ccagtaacgt tatacgtat cgcagagttt gcccgtgtct  
1141 cttatcagac ctttccgcgtt gtggtaacc aggcagcca ctttctcgat aaaaacgcggg  
1201 aaaaagtggaa agcggcgatg gcgagactga attacattcc caaccgcgtt gcacaacaac  
1261 tggccggccaa acagtcgtt ctgattggcg ttggccaccc cagtctggcc ctgcacgcgc  
1321 cgtcgcataat tgcgtggcg attaaatctc gcccgcgtt actgggtgcc agcgtgggt  
1381 tgtcgatggtaatgtgaaa agaacgaagc ggcgtcgaaat cctgtaaagc ggcggcgtac aatcttcgt  
1441 cgcaacgcgtt cagtggctg atcattaaact atccgcgttga tgaccaggat gcaattgcgt  
1501 tggaaagctgc ctgcactaat gttccggcg tatttctgtat tgcgtctgtat cagacacccca  
1561 tcaacagtat tattttctcc catgaagacg gtacgcgtt gggcgtggag catctggcg  
1621 cattgggtca ccagcaaaatc ggcgtttag cggcccgatt aagttctgtc tcggccgcgt  
1681 tgcgtctggc tggctggcat aaatattca ctgcgttca aattcagccg atagcggaaac  
1741 gggaaaggcga ctggagtgcc atgtccgggtt ttcaacaaac catgcaatgt ctgaatgagg  
1801 gcatgttcc cactgcgtatg ctgggttccaa acgatcgat ggcgtggc gcaatgcgc  
1861 ccattaccga gtccggcgat cgcgttggcg cggatatctc ggttagggta tacgacgata  
1921 ccgaagacag ctcatgttattt atccccgtt taaccaccat caaacaggat tttcgctgc  
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2041 atcagctgtt gcccgtctca ctggtaaaaa gaaaaaccac cctggcgccc aatacgcaaa  
2101 ccgcctctcc cccgcgtt gcccgttcat taatgcgtt ggcacgcacag gttccgcac  
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2221 caggcttac actttatgtt cccgcgttgc aagaacctca cgtcagggtt cactttcggt  
2281 gggaaatgtgc gggaaaccccg tatttgggtt tttttctaaa tacattcaaa tatgtatccg  
2341 ctcatgagac aataaccctgtt ataaatgtt caataatatt gaaaaaggaa gagttatgt  
2401 attcaacatt tccgtgtcgcc ctttttttttgcgtt ctttttttttgcgtt tcctgttttt  
2461 gctcaccctggaaacgcgtt gaaatggaaatgtgtt gatgtgtt gtcacgcac  
2521 ggttacatcg agaactggat ctcaacacgcgtt gtaagatctt tgaggtttt cggccggaa  
2581 aacgtttcc aatgtatgtt gtttttttttgcgtt tggccggta ttatcccgtt  
2641 ttgacgcgg gcaagagcaat ctcggcgcc gcatacacta ttctcagaat gactttgggtt

Fig. 13B



2701 agtactcacc agtcacagaa aagcatctta cgatggcat gacagtaaga gaattatgca  
 2761 gtgctccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcgag  
 2821 gaccgaagga gctaaccgct ttttgacaca acatggggta tcatgtact cgccttgatc  
 2881 gttggaaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatccg  
 2941 tagcaatggc aacaacgttgcg cacaactat taactggcga actacttact ctatctccc  
 3001 ggcaacaatt aatagactgg atggaggcgg ataaagtgc aggaccactt ctgcgctcgg  
 3061 ccctccggc tggctgggtt attgctgata aatctggac cggtgagcgt gggctcg  
 3121 gtatcattgc agcaactggg ccagatggta agccctcccg tatactgtt atctacacga  
 3181 cggggagtca gcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac  
 3241 tgattaagca ttggtaactg tcagaccaag ttactctata tatactttat attgattaa  
 3301 aacttcattt ttaatttaaa agatctagg tgaagatcct ttttataat ctcatgacca  
 3361 aaatccctta acgtgatgtt tcgttccact gagcgtcaga cccctgtagaa aagatcaaag  
 3421 gatctcttg agatccctttt ttctgcgcg taatctgctg ctgcacaaaca aaaaaaccac  
 3481 cgctaccagc ggtggttgtt ttgcggatc aagagctacc aactctttt ccgaaggtaa  
 3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agttagccg tagttaggcc  
 3601 accacttcaa gaactctgta gcacccgcta catacctcgc tctgctaatt ctgttaccag  
 3661 tggctctgc cagtggcgat aagtctgtc ttaccgggtt ggactcaaga cgatagttac  
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 3781 gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcctc  
 3841 ccgaaggggag aaaggcgac aggtatccgg taagcgccag ggtcggaaca ggagagcgca  
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 3961 tctgacttgc gctgcattt ttgtatgtc cgtcaggggg gcggagccata tggaaaaacg  
 4021 ccagcaacgc ggccctttta cgggtcctgg cctttgcgt gcctttgtc cacatgttct  
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 4381 aaggcgcaact cccgttctgg ataattttt ttgcggcgc atcataacgg ttctggcaaa  
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 5341 tgcggccctc ctccctactc agctctgtt gggccaggctt gactggcgat cggaggctcg  
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 5461 ggcgtgccccca ggcgtactgg caaatggcgc ccctgtttctt ggagctgctt gggaaaccacg  
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Fig. 13C



5581 cagcagccgg tgcgtgtgcc cgggagaagc cccaggcgtc tggcgccccc cccgaggagg  
5641 aggacacaga ccccccgtcgc ctgggtcagc tgctccgcga gcacaggcgc cccgtggcagg  
5701 tgtacggctt cgtgcgggcc tgcctgcgcg ggctgggtcgc cccaggcctc tgggctcca  
5761 ggcacaacga acggcccttc ctcaggaaca ccaagaagtt catctccctg gggaaagcatg  
5821 ccaagctctc gtcgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc  
5881 gcaggagccc aggggttggc tgcgttccgg cccgcagagca cccgtctgcgt gaggagatcc  
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7441 tttccccccag ggatgtcgtt gggggccaaag ggccggccggc gcccctgcctt ctcggaggcc  
7501 gtgcgttggc tgcgttccca agcattccgt ctcaagctga ctcgcacccgg tgcacccatcc  
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*Fig. 13D*

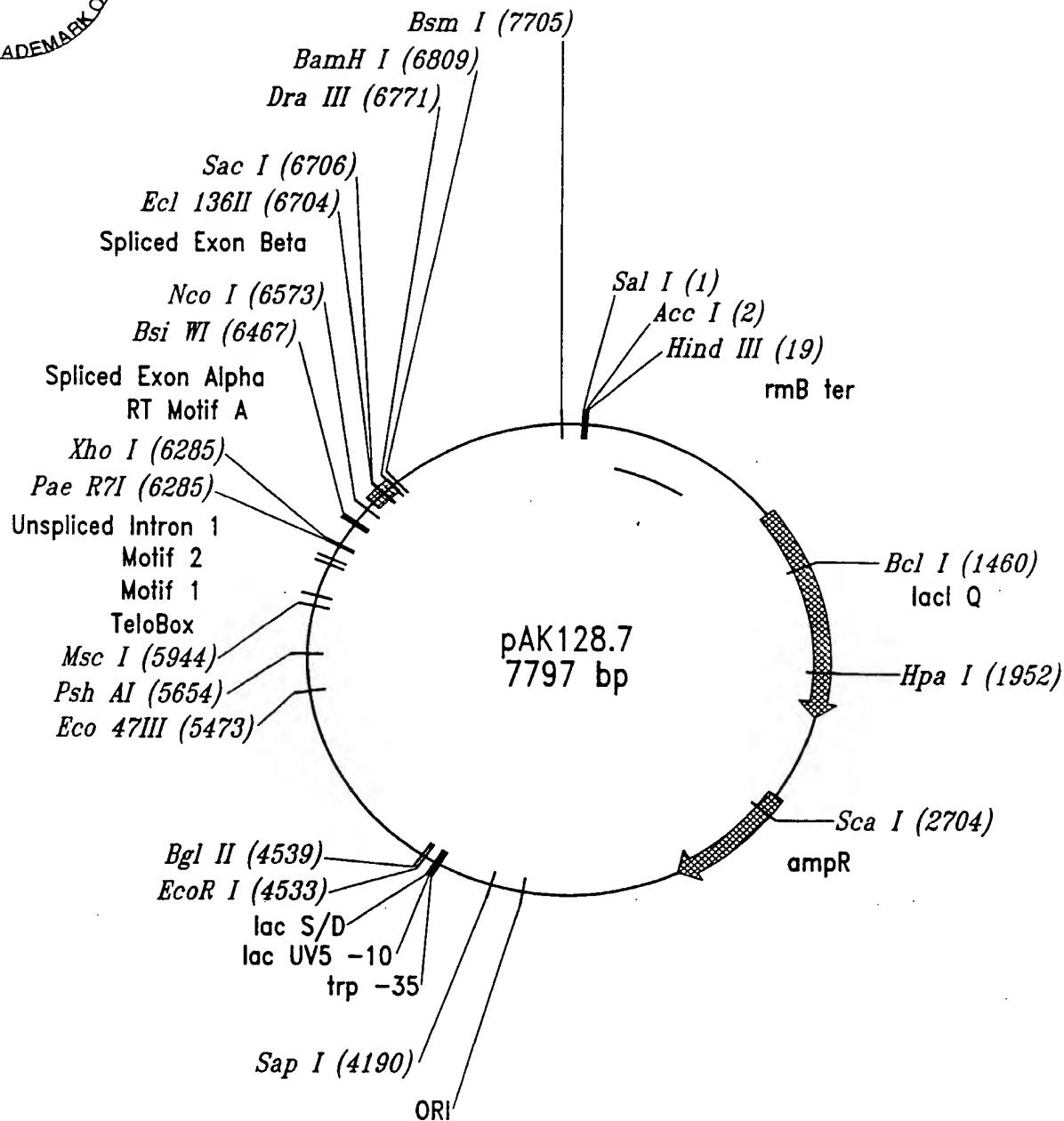


Fig. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular  
DEFINITION Human telomerase clone with alternative C-terminus

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61 aaccctggcg ttacccaaact taatcgccctt gcagcacatc ccccttcgc cagctggcg  
121 aatagcgaaag aggcccccac cgatcgccct tcccaacagt tgccgacgct gaatggcgaa  
181 tggccctgaa tgcgttattt tctccttacg catctgtcg gtatttcaca ccgcataaaat  
241 tccctgtttt ggccgatgag agaagatttt cagcctgata cagattaaat cagaacgcag  
301 aagcggctcg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cactgcaccc  
361 catgcccgaac tcagaagtga aacggcgtag cgccgatggt agtgtgggt ctccccatgc  
421 gagagtaggg aactgcccagg catcaaataa aacgaaaggc tcagtgcggaa gactgggcct  
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541 cgaggatggaa cggtgcgaag caacggcccg gaggggtggcg ggcaggacgc ccggccataaa  
601 ctggccaggca tcaaattaag cagaaggcca tcctgacggta tgccctttt gcgttctac  
661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacgta aactagcctc  
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Fig. 14B



Fig. 14C



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Fig. 14D

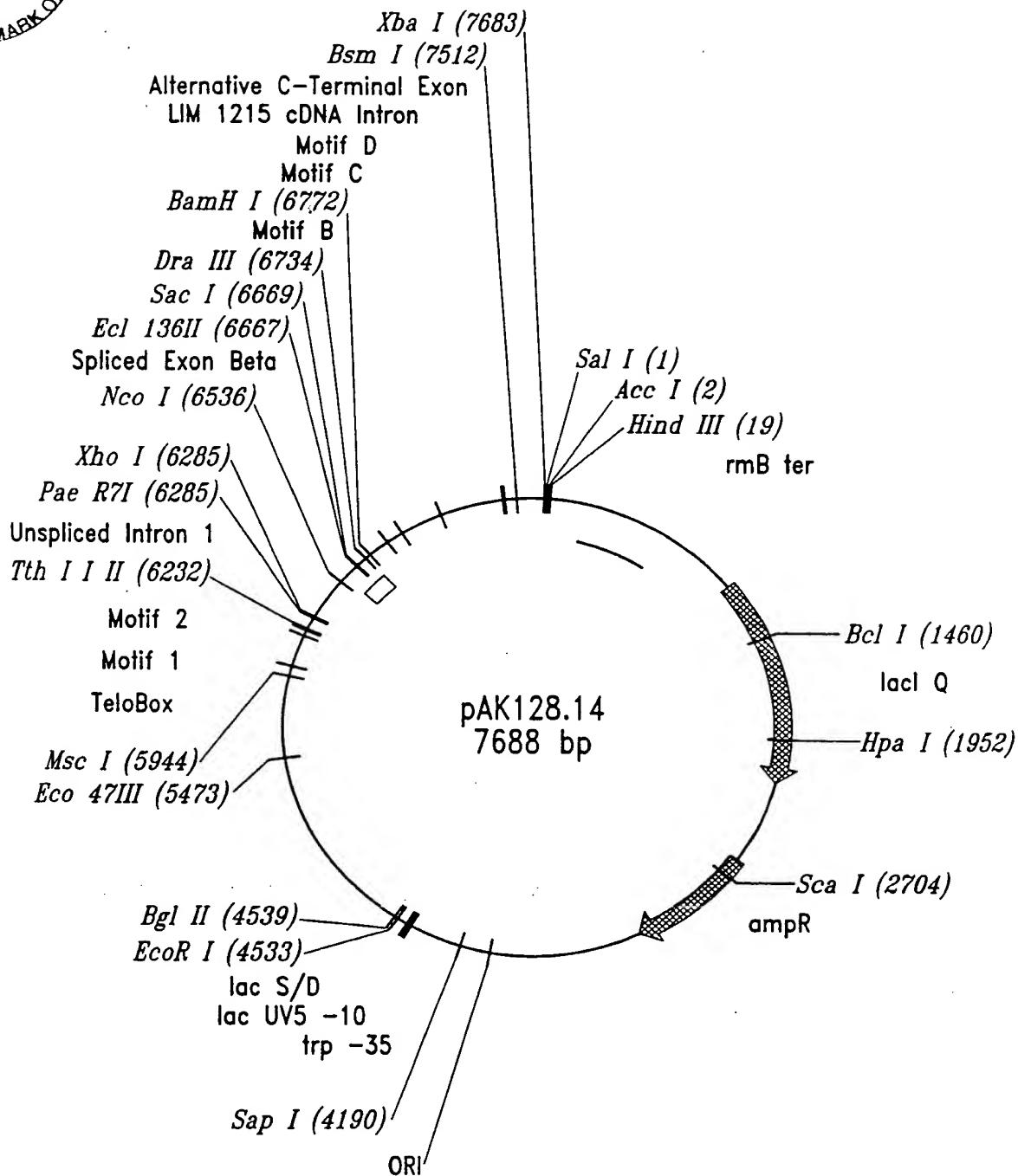


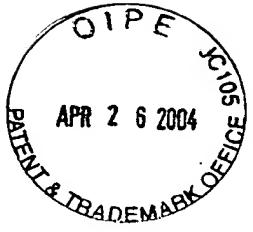
Fig. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular  
DEFINITION Human telomerase clone with exon alpha spliced out

A circular stamp with the words "U.S. PATENT & TRADEMARK OFFICE" around the perimeter. The center contains the date "APR 26 2004" and the serial number "5010152".

1 tcgacctgcg ggcatgcaag ctggcactg gccgtcgaaa tacaacgtcg tgactggaa  
61 aaccctggcg ttacccaact taatgcgcctt gcagcacatc ccccttcgc cagctggcgt  
121 aatagcgaag aggcccac cgcgcgcctt tcccaacagt tgccgagcct gaatggcgaa  
181 tggcgcctga tgcggattt tctcgcctt cgcgcgcctt cgcgcgcctt ccccttcgc cagctggcgt  
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481 ttcttttat ctgttgcctt tcgggtgcacg ctctctgtgc taggacaaat ccccccgc  
541 cggatttgcg cgttgcgaag caacgcgcgt aacgcgcgt aacgcgcgt aacgcgcgt  
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661 aaactcttc tgcgcgcctt ctcgcgcgt aacgcgcgt aacgcgcgt  
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2581 aacgtttcc  
2641 ttgcgcgcgtt

Fig. 15B



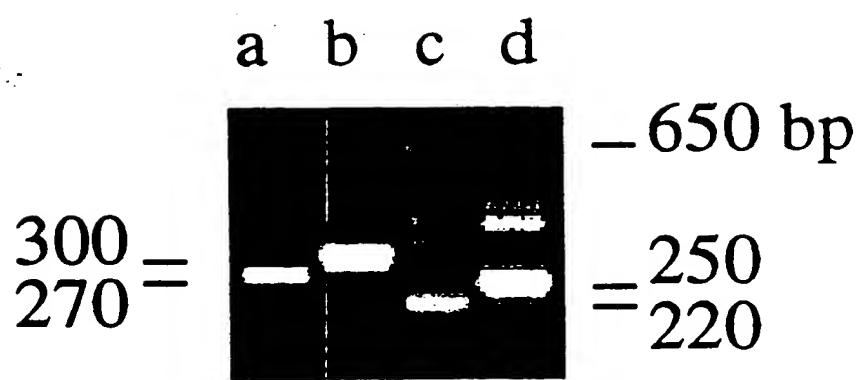
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Fig. 15C



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7621 tgccctggag gcccgcagcca acccggcaact gcccctcagac ttcaagacca tcctggactg  
7681 atcttagag

*Fig. 15D*



*Fig. 9*



sequence "Y" 104-105 bases

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGCCGGGGGAACCAAG  
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln  
AlaSerProGlySerAlaSerGlyTrpGly\* GlyArgProGlyGlyThrSer  
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG  
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg  
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly  
ThrCysGlyGluGlnArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTGTTAACCTCCTTTAACAGAA  
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases

GTGGATGTGACGGCGCGTACGACACCATCCCCAG  
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGCTCACCTG  
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCCTCCTG  
GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeu

AATGAGGCCAGCAGTGGCCTTCTCGACGTCTCCTACGCTTCATGTGCCACCAC  
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA  
AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGCAGGTGCTGCAG  
Ter

GGCGTTCGTCACCTCTGCTTCCGTGTTGGCAGGGACTGCCAATCCAAAGGGT  
CAGATGCCACAGGGTGCCCTCGTCCATCTGGGCTGAGCACAAATGCATCTTCTG  
TGGGAGTGAGGGTGCCTCACACGGGAGCAGTTCTGTGCTATTTGGTAA...



sequence "3" 159 bases

CGAAGAAAACATTCTGCGTGAECTCCTGCGGTGCTTGGTGGGACAGCCAGAG  
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGCAGCTTCCGGTGTCTCCTGGGAGG  
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGAECTCCTCAGCCTCTGTTTCCCCAG  
GlyValGlyLeuGlyLeu \*

sequence "X" unknown length

...GACAGTCACCAGGGGGGTTGACCGCCGGACTGGCGTCCCCAGGGTTGACTATAGGA  
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGCTCTCAGAGGCCTGGCTGGCATGG  
GTGGACGTGGCCCCGGGCATGGCCTCTGCGTGTGCCGTGGTGCCTGAGCCCT  
CACTGAGTCGGTGGGGCTTGTGGCTCCCGTGAAGCTTCCCCTAGTCTGTTGTCTGG  
CTGAGCAAGCCTCTGAGGGCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)  
GTGGCTGTGCTTGGTTAACCTCCTTTAACCAAGAAGTGCCTTGAGCCCCACATT  
TGGTATCAGCTTAGATGAAGGGCCCGAGGAGGGCCACGGGACACAGCCAGGGCCAT  
GGCACGGCGCCCACCCATTGTGCGCACAGTGAGGTGGCGAGGTGCCGTGCCTCCA  
GAAAAGCAGCGTGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

*Fig. 10B*



### Truncated telomerase

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M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGCGCCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGGCTGCCCTGGACGCACGGCCGCCCCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCTCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCAGCGCGCCGAAGAACGTGCTGGCTTCGGCTGCCCTGGACGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGCCTGCTGCCCTGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTCACCTGCTGGCACGCTGCCGCTTTGTGCTGGCTCCAGCTGCCCTACAGGTGTGCCGGCCCGCTGTACAGCTGGCGCTGCCACTCAGCCGGCCCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGGACCCGAAGGCCTGGGATGCAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGGCTGCCAGCCGGTGCAGGGAGGCCGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTGTGCCGTTGCCAACAGGGCCAGGCCTGGCCTGCCCTGAGCGGAGCCGGTGGCCAGGGCTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGACCG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGTTGTACCTGCCAGACCCCGAACAGGAAAGCCACCTTTGGAGGGTGCCTCTGGCACCGCCTCCACCCATCCGTGGCCCGCAGCACACGCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGGGCACACAGTCCCTGGACACGCTTGTCCCGGTGACGCCAGACCAAGCCTCTACTCCCTCAGGCAGACAGCTGCCCTCTCCACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCTGACTGGCCTGGAGGCTGAGGACCACTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGGGGCCCTGTTCTGGAGCTGCTGGAACACCGCAGTGGCCCTACGGGTGCTCTAACAGCAGCTGCCCTGGAGCTGCCAGCAGGGTGTCTGGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCCAGGGCTGTGGCCGCCAGGCCAGGGAGGAGGACACAGACCCCGTCGCTGGAGCTGCCAGGGCTGGAGGTGACGGCTCGCTGCC  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGGCCGGCTGGTGGCCCTAGGCCTCTGGGCTCCAGGCACAACGAACGCCGTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAGATGAGCGTGCAGGGACTGCGCTGGCTGCCAGGAGCCAGGGTGGCTGTTCCGGCCAGAGCACCGCTCGCTGAGGAGATCCTGGCAAGTTCCTGCAGGAGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTACGTCGTCAGCTTCTTATGTCACGGAGACACGTTCAAAGAACAGGCTTTTCTACCGGAAGAGTGTGGAGCAAGTGGCAAGTGGCAAGCTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
  
AAT--NNN--GACAGTCACCGGGGTTGACCGCCGGACTGGCGTCCCCAGGGTGACTATAGGACCAAGGTGCTGCCCTGCAAGTAGAGGGCTCTAGAGGCCTGGCTGG

*Fig. 11A*



CATGGGTGGACGTGGCCCCGGGATGGCCTCTGGCTGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGCTTGTGGCTCCCGTGAGCTTCCCCTAGTCTGTGTC

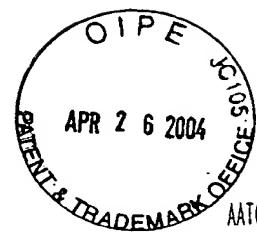
*Fig. 11B*



### Truncated protein 1

ATGCCGCGCGCTCCCCGTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGGCCACGTC  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGCGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGGACCCGGCGCTTCCCGCGCTGGTGCCAGTGCTGGTGCCTGGCTGCCCTGGACGCACGGCCGCCCCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P H D A R P P P A A  
  
CCCTCTTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGCCCGAGTGCTGCAGAGGTGTCGAGCGCGCCGAAGAACGTCCTGGCTTCCGCTGCTGGACGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
GGGGGGCCCCCGAGGCCTTACCAACCGCGCTACCTGCCAACACGGTGACCGACGCACTGGGGGAGGGGGCTGGGGCTGCTGCTGGCCCGTGGCGACGACG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTCACCTGCTGGCACGCTGCCGCTTTGTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCCGCTGCTACAGCTGGCGTCCACTCAGGCCCCGGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGGACCCGAAGCGTCTGGATGCAACGGCCTGGAACCATAGCTCAGGGAGGCCGGTCCCTGGCCTGCCAGCCCCGGTGCAGGGAGGCCGG  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCGTTGCCAACAGGGCCAGCGTGGCTGCCCTGAGCCGGACCCGTTGGCAGGGCTCTGGCCACCCGGCAGGACGCCGAGTGC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGTTGTCACCTGCCAGACCCGCCAGAGACCCGCCAGAGAACCCACTTTGGAGGGTGCCTCTGGCACCGCACTCCACCCATCCGTGGCCGCCAGCAC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGGGCCACACGCTCCCTGGACACGCCCTGTCCCCCGTGTACGCCAGACCAAGCACTTCTACTCCCTCAGGCACAAAGGAGCAGCTGCCCTCTTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCCTGACTGCCGCTGGAGGCTCGTGGAGACCATTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCCCAGGTTGCCCTGCCAGGCC  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y H Q  
  
AATGGGGCCCTGTTCTGGAGCTGCTGGAACCAAGGCCACTGCCCTACGGGTCTCTCAAGACGCACTGCCGCTGGAGCTGCCCTACCCAGCAGGGTGTCTGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGGCCAGGGCTGTGGCGCCCGAGGAGGAGACACAGACCCCGTCGCTGGTGCAGCTGCCAGCACGCCCTGGCAGGTGACGGCTCGTGC  
E K P Q G S V A A P E E E D T D P R R L V O L L R O H S S P W Q V Y G F V R A C  
  
CCTGCCGGCTGGTGCCTGCCAGGCACAACGAAACGCCGCTCCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAGCTGCC  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCGCTGCCAGGGAGATC  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTACGTCGAGCTGCTAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACGGCTTTCTACCGGAAGAGTGTCTGGAGCAAGTGC  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11C



AATCAGACAGCACTGAAGAGGGTGCAGCTGCAGGAGCTGTCGGAAAGCAGAGGTCAAGCAGCATCGGGAAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGGTTGGTTAACCTCCCTTTAACCGAGAA  
V A V L W F T F L F N Q K

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGTCTCACCTCGAGGGTGAAGGCACTGTTAGCGTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G \*

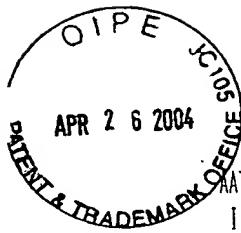
*Fig. 11D*



Truncated protein 2

ATGCCGGCGCTCCCCGTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGTGGCACGTCGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGCGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCGTGGTGGCCAGTGCCTGCTGTGCGTGCCTGGCACGCCGCCCCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCCCTTCCCCCAGGTGCTCGCTGAAGGAGCTGGTGGCCAGTGCTGCAGGGCTGTGCGAGCGCGCCGAAGAACGTCGCTGGCTTGGCTCGCTGCTGGACGGGCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTTACCAACAGCGTGGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGGCTGCTGCGCCGCTGGCGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTCACCTGCTGGCACGCTGGCCTTGTGCTGGCTCCAGCTGCCTACCAAGGTGCGCCGCTGCTGCGCTGCGCCGCTGCTGCGCCGCTGCCACTCAGGCCGGCCCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGACCCCGAAGGCCCTGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCCGGTGCAGGGAGGCCGGCAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGCTGCCCTGCCAACAGGCCAGGGCTGGCCTGAGCCGGAGGCCGCTGGCAGGGCTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAACAGCCACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGGGGCCAGCACACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGGGCCACCACGCTCCCTGGACACGCCCTGTCCCCGGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCAGAACGGAGCAGTCGGCCCTCTTCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTAGGCCAGCTGACTGGCTCGGAGGCCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGCCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGAACACAGCGCAGTCCCTACGGGTGCTCTCAAGACCAACTGCCGCTGCGAGCTGCCAGCCAGCAGCCCTGGCAGGTGACGCCCTGCG  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCCAGGGCTCTGGCGGCCCGAGGGAGGGACACAGACCCCGTCGCTGGCAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGCCCTGCG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCGGCTGGTGCCCAAGGCCCTGGGCTCCAGGCACAAGAACGCCCTCTCAGGAACACCAAGAACGTCATCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAGATGAGCGTGGGACTGCGCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGCTGCCGTGAGGAGATCTGCCAAGCTCGCTGCCAGGAGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTCGAGCTGCTCAGGTCTTCTTGTACGGAGACCAAGCTTCAAAAGAACGGCTTTTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L O S I G

Fig. 11E



ATCAGACAGCACTGAAGAGGGTCCAGCTGGGGAGCTGTCGAAGAGGTCAAGCAGCATCGGAAGCCAGGGCCGCCCCTGCTCACGTCCAGACTCCGCTTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGGGCCATTGTGAACATGGACTACGTCTGGAGCCAGAACCTTCCCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTAAGGCAGTGTTCAGCGTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
GGGGCCGGCCGGCCGGCCCTCTGGGCCCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGCACCTCGTGTGCTGCGGTGCGGGCCAGGACCCGCCGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAGGACAGGCTACGGAGGTACGCCAGCATCATAAACCCCAGAACACGTACTGCCGTGCGTCGGTATGCCGTGGTCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V O  
GAAGGCCGCCATGGCACGTCCGAAGGCCTCAAGAGCCAC  
K A A H G H V R K A F K S H

GTCTACGTCAGTG  
V L R P V

CGAGGGATCCGCAGGGCTCCATCCTCCACGCTCTGAGCCTGTGCTACGGCACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCCTGGTGG  
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G  
TGATTTCTTGTGGTACACCTCACCTACCCACGCAGAACCTTCAGGACCTGGTCCGAGGTCTCTGAGTATGGCTGCGGTGAATTGCGGAAGACAGTGGTGAATTCCC  
\*

*Fig. 11F*



Reference protein

|  |     |
|--|-----|
| ATGCCGCGCTCCCCCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG    | 60  |
| MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu | 20  |
| GTGCTGCCGCTGGCCACGTTCTGCGGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG | 120 |
| ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln | 40  |
| CGCGGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCTGGTGTGCGTGCCTGG       | 180 |
| ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp | 60  |
| GACGCACGGCCGCCCGCGCCCCCTCCTCCGCCAGGTGTCCTGCCTGAAGGAGCTG      | 240 |
| AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 80  |
| GTGGCCCAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGAAGAACGTGCTGGCCTTCGGC   | 300 |
| ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly | 100 |
| TTCGCGCTGGACGGGCCCAGGGGGCCCCGAGGGCCTTCACCACCGCGTGC           | 360 |
| PheAlaLeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArg    | 120 |
| AGCTACCTGCCAACACGGTGACCGACGCCTGCGGGGGAGCGGGGCGTGGGGCTGCTG    | 420 |
| SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu | 140 |
| TTGCGCCGCTGGACGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCCTTTGTG  | 480 |
| LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal | 160 |
| CTGGTGGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGTGTACCAGCTGGCGCT    | 540 |
| LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 180 |
| GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTGGGATGCGAA     | 600 |
| AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu       | 200 |
| CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCCTGCCAGCCCCGGT   | 660 |
| ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 220 |
| GCGAGGAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT     | 720 |
| AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 240 |
| GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGTCTGGGCCACCCGGC       | 780 |
| GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 260 |
| AGGACCGGTGGACCGAGTGACCGTGGTTCTGTGTTGTCACCTGCCAGACCCGCGAA     | 840 |
| ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 280 |
| GAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGC          | 900 |
| GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 300 |

Fig. 11G



|  |             |
|--|-------------|
| CGCCAGCACCACGCCGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCC<br>ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro   | 960<br>320  |
| TGTCCCCCGGTGTACGCCAGACCAAGCACTTCCTCTACTCCTCAGGCCACAAGGAGCAG<br>CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln  | 1020<br>340 |
| CTGCCGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC<br>LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu     | 1080<br>360 |
| GTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCC<br>ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro    | 1140<br>380 |
| CGCCTGCCCAAGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC<br>ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis       | 1200<br>400 |
| GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTCGGTCA<br>AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr       | 1260<br>420 |
| CCAGCAGCCGGTGTCTGTGCCCGGGAGAACGCCCCAGGGCTCTGGCGGGCCCCGAGGAG<br>ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu  | 1320<br>440 |
| GAGGACACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG<br>GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln   | 1380<br>460 |
| GTGTACGGCTTCGTGGGGCCTGCCTGCGCCGGCTGGTGCCTGGGGCTCTGGGGCTCC<br>ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer    | 1440<br>480 |
| AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGAAGCAT<br>ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 1500<br>500 |
| GCCAAGCTTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTTGGCTG<br>AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu  | 1560<br>520 |
| CGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC<br>ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle   | 1620<br>540 |
| CTGGCCAAGTTCTGCACTGGCTGATGAGTGTGACGTCGTCAGCTGCTCAGGTCTTC<br>LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe     | 1680<br>560 |
| TTTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTC<br>PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal        | 1740<br>580 |
| TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGCAGCTGCC<br>TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu      | 1800<br>600 |
| CTGTGGAAAGCAGAGGTCAAGGCAGCATTGGGAAGGCCAGGCCCTGCTGACGTCCAGA<br>LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg   | 1860<br>620 |

*Fig. 11H*



|  |             |
|--|-------------|
| CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG<br>LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal       | 1920<br>640 |
| GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA<br>GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla       | 1980<br>660 |
| CTGTTCAGCGTGCCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGCGCCTCTGTG<br>LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal        | 2040<br>680 |
| CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGCCTGCGTGTGCGGGCCAG<br>LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln        | 2100<br>700 |
| GACCCGCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC.<br>AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle         | 2160<br>720 |
| CCCCAGGACAGGCTCACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGC<br>ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys         | 2220<br>740 |
| GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGCACGTCCGCAAGGCCTCAAG<br>ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys          | 2280<br>760 |
| AGCCACGTCTCACCTTGACAGACCTCAGCGTACATGCGACAGTTGTGGCTCACCTG<br>SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu           | 2340<br>780 |
| CAGGAGACCAGCCGCTGAGGGATGCCGTCGTACAGCAGAGCTCCTCCCTGAATGAG<br>GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu              | 2400<br>800 |
| GCCAGCAGTGGCCTTCGACGTCTTACGCTTACGCTTACGCTTACGTGCCACCACGCCGTGCGCATC<br>AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle | 2460<br>820 |
| AGGGGCAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG<br>ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu        | 2520<br>840 |
| CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGATTGGCGGGAC<br>LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp            | 2580<br>860 |
| GGGCTGCTCCTGCGTTGGATGATTCTTGGTACACCTCACCTCACCCACGCG<br>GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla                | 2640<br>880 |
| AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG<br>LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu       | 2700<br>900 |
| CGGAAGACAGTGGTGAACCTCCCTGTAGAACGAGACGAGGCCCTGGTGGCACGGCTTTGTT<br>ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal      | 2760<br>920 |
| CAGATGCCGGCCACGGCCTATTCCCTGGTGCAGGCCTGCTGCTGGATACCCGGACCTG<br>GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuAspThrArgThrLeu            | 2820<br>940 |

*Fig. 11I*



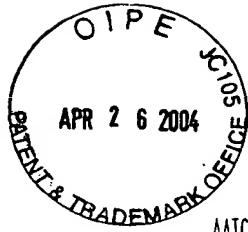
|   |              |
|---|--------------|
| GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTC<br>GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe  | 2880<br>960  |
| AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGGGCTG<br>AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu   | 2940<br>980  |
| AAGTGTACAGCCTGTTCTGGATTTGCAGGTGAAACAGCCTCAGACGGTGTGCACCAAC<br>LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn  | 3000<br>1000 |
| ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCA<br>IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro  | 3060<br>1020 |
| TTTCATCAGCAAGTTTGGAGAGAACCCCACATTTTCTGCGCGTCATCTGACACGGCC<br>PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla   | 3120<br>1040 |
| TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC<br>SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly | 3180<br>1060 |
| GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC<br>AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu | 3240<br>1080 |
| AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG<br>LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln  | 3300<br>1100 |
| ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC<br>ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn    | 3360<br>1120 |
| CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC<br>ProAlaLeuProSerAspPheLysThrIleLeuAsp  | 3420<br>1132 |



### Truncated protein 3

ATGCCGCGCCTCCCCCTGCCAGCCGTGCCCTCCCGCAGCCACTACCGGAGGTGCTGCCCTGCCACGTTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGGCCCTGGGGCCCAGGGCTGGCGCTGGTCAAGCGGGGACCCGGCGCTTCCGCGCTGGGGCCAGTGCTGGTGTGCGTGCCCTGGGACGACGGCCGCCCCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCCCTCCGCCAGGTGCTCCGCTGAAGGAGCTGGTGGCCCGAGTGCTGAGAGGCTGTGCGAGCGCCGCGGAAGAACGTCGCTGGCTTCGCGCTGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGTACCTGCCAACACGGTACCGACGCAGTGGGGAGCGGGGCTGCTGCTGCCGCTGGGACGAGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTCACCTGCTGGCACGCTGGCTCTTGCTGGCTCCAGCTGCCCTACCAAGGTGCTGGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGGCCCCGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGGGACCCGAAGGGCTGGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGCTGCCAGCCCCGGTGCAGGGAGGCCGGGGCAGTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R R G G S A  
  
CAGCCGAAGTCTGCCCTGCCAACAGAGGCCAGGGCTGGCGCTGCCCTGAGCCGGAGGCCGTTGGCAGGGTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGC  
S R S L P L P K R P R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGTTGTCACCTGCCAGACCCCGAACAGAGGCCAGGGCTGGCGCTCTGGAGGGTGGCTCTGGCACGCCACTCCACCCATGGCCGCCAGCACACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATGCCGCCACCACGCCCTGGGACACGCCCTGGCTCCCGGTGACGCCAGAACACTCTCTACTCCCTAGCGACAAGGAGCAGTCGGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGGAGAACATCTTCTGGGTCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGGCCCTGCCAGCGCTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCACGCCAGTCCCTACGGGTGCTCTCAAGACCAAGCAGCCGCTGCCAGCTGCCAGGGTACGGCTCGTGCAGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGGCCAGGGCTCTGGCGGCCAGGGAGGACACAGACCCCGTCGCTGGAGAACATCTGGGCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAGCTCGCTGCCAG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCGCCGCTGGTGCCTGCCAGGCCCTGGGCTCCAGGAACACGAACGCCGCTCTCAAGAACAGGAGATCTGGCAAGTCTGGCCAGCTGGCTGCCAG  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGGAGGCCAGGGTGGCTGTTCCGGCCAGAGCACCGTGCAGGGAGATCTGGCAAGTCTGCAG  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTGAGCTGCTGAGCTGCTAGGTCTTCTTATGTCACGGAGACCAAGCTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTGCTGGAGCAAGTTGCAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

*Fig. 11K*



AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGACGTCTGGAAAGCAGAGGTCAAGGCAGCATGGGAAGCAGGCCCCCTGCTGACGTCCAGACTCCCTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
C G G G C T G C G G C C G A T T G T G A A C A T G G A C T A C G T C G T G G G A G C C A G A A C G T C C G C A G A A A A G A G G G C C G A G G G T C T C A C C T C G A G G G T G A A G G C A C T G T C A G C G T G C T C A A C T A C G A  
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
G C G G G C G C G G C C C C G C C T C T G G G C C T C T G T G C T G G G C T G G A C T A T C C A C A G G G C T G G G C A C C T C G T G C T G C G T G T G C G G G C C C A G G A C C C G C C T G A G G C T G A C T T  
R A R R P G L L G A S V L G L D I H R A W R T F V L R V R A Q D P P P E L Y F  
T G T C A A G G T G G A T G T G A C G G G C C G T A C G A C A C C A T C C C C A G G A C A G G G C T A C G G A G G T C A T C G C C A G C A T C A T C A A A C C C A G A A C A C G T A C T G C G T G C G T C G T A T G C C G T G G T C C A  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P O N T Y C V R R Y A V V Q  
G A A G G C C G C C C A T G G G C A C G T C C G C A A G G C C T T C A A G A G C C A C G T C T C A C C T G A C A G A C C T C C A G C C G T A C T G C G A C A G T T C G T G G C T C A C C T G C A G G A G A C C A G C C C G C T G A G G G A  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
T G C C G T C G T C A T C G A G C A G A G C T C C T C C T G A A T G A G G C C A G C A G T G G G C T T C G A C G T C T C C T A C G C T T C A T G T G C C A C C A C G C C G T G C G C A T C A G G G G C A A G T C C T A C G T C C A G T G  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
C C A G G G A T C C C G C A G G G C T C C A T C C T C C A C G C T G C T G C A G C C T G T G C T A C G G C G A C T G G A G A A C A A G C T G T T G C G G G G A T T C G G C G G A C G G G C T G C T C C T G C G T T G G T G G A  
Q G I P Q G S I L S T L L C S L C Y G O M E N K L F A G I R R D G L L L R L V D  
T G A T T T C T T G T T G G T G A C A C C T C A C C T C A C C C A C G C G A A A C C T C C T C A G G A C C C T G G T C C G A G G T G T C C C T G A G T A T G G C T G C G T G G T G A A C T T G C G G A A G A C A G T G G T G A A C T T C C  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
T G T A A G A A G A C G A G G G C C T G G G T G G C A C G G C T T T G T C A G A T G C C G G C C A C G G C C T A T T C C C T G G T G C G G C C T G C T G C T G G A T A C C G G A C C C T G G A G G T G C A G A G C G A C T A C T C C A G  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R  
G T G A G G C C A C T T G G C C G G A A G T G G A G C C T G T G C C C G C T G G G C A G G T G C T G C A G G G C C T T G C G T C C A C C T C T G C T T C C G T G T G G G G C A G G C A C T G C C A A T C C C A A A G G G T C A G A  
\*  
T G C C A C A G G G T G C C C T C G T C C C A T C T G G G G C T G A G C A C A A T G C A T C T T T C T G T G G G A G T G A G G G T G C C T C A C A A C G G G A G C A G T T T C T G C T G T A T T T G G T A A ...

Fig. 11L



Altered C-terminus protein

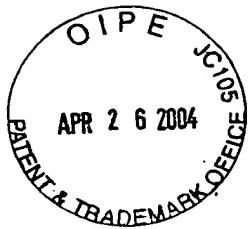
ATGCCGCCGCTCCCCCTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGGCACCTCGT  
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
 CGGCCCTGGGCCCCAGGGCTGGCGCTGGTCAGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGACGCACGGCCGCCCCGGCG  
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
 CCCCTCTCCGCCAGGTGCTCTGCCAGGGCTGGCCAGTGCTGAGGGCTGCGAGCGCCGCGAAGAACGTGCTGGCTTCGCTCGCCTGGACGGGGCC  
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
 CGGGGGCCCCCGAGGCCTCACCAACAGCTGCGCAGTACCTGCCAACACGGTACCGACGCAGTGGGGGAGCGGGGCTGGGGCTGCTGCGCCCGTGGGACGACGT  
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
 GCTGGTTACCTGCTGGCACGCTGCGCTCTTGCTGGCTCCAGCTGCCCTACCAAGGTGCGGGCCGCGCTGACCGCTCGCCGCTGCCACTCAGGCCGGCCCCCG  
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
 ACACGCTAGTGGACCCGAAGGCCTGGGATGCCAACGGGCTGGAACCATAGCCTAGGGAGGCCGGCTGGGCTGCCAGGCCGGGTGGCCCTGGGCTGCCAGGCCGGGTGCGAGGAGGCGGGGGAGTGC  
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
 CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGGGCTGGCGCTGCCCTGAGCCGGAGGCCGGCTGGGAGGGTCTGGCCACCCGGGAGGACGCCGGTGGGACCGAGTGCACCG  
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
 TGGTTCTGTGTGGTGTACCTGCCAGACCCGCCAGAACGCCACCTCTTGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGGCCGGCCAGCACCCAGCGGGCCCC  
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
 ATCCACATGCCGCCACACGCCCTGGACACGCCCTGTCGCCCTGAGGCCACTCCCTACTCCAGCCAGAGGCCACTCCCTACTCCAGCCAGAGGCCACTCCCTACTCCAG  
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
 CTCTGAGGCCAGCTGCTGGAGCTGGCGCTGGAGGCTGTGGAGACCATCTTGAGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCCTGCCAGCGTACTGGCA  
 S L R P S L T G A R R L V E T I F L G S R P H M P G T P R R L P R L P Q R Y W Q  
  
 AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTGCCTACGGGGTCTCTCAAGACGCACTGCCGAGCTGCCAGGGTCAACCCAGCAGCCGGTGTCTGCC  
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
 GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGGAGGGACACAGACCCCGTCCCTGGTCAGCTGCCAGCACAGCAGGCCCTGGCAGGTGACGGCTCGTGGCCCTG  
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
 CCTGGCCGGCTGGTGCCTCCAGGCCCTGGGCTCCAGGCACACGAACGCCCTCCAGGAACACCAAGAAGTCTCCCTGGGAAGCATGCCAGCTCGTGCAGGAGCT  
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
 GACGTGGAAAGATGAGCGTGCAGGACTGCGCTGGCTGCGCAGGAGGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGCTGCGTGAAGGAGATCTGGCAAGTCTGCACTGGCT  
 T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
 GATGAGTGTGACGTGCTCGAGCTGCTCAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAGAACAGGCTTCTACCGGAAGAGTGTCTGGAGCAAGTGTGCAAAGCATGG  
 M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

*Fig. 11M*



AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGAGCTGTGGAAAGCAGAGGTCAAGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCAGACTCGCTTCATCCCCAAGCTGA  
I R O H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
  
CGGGCTGGGGCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTTCAGCGTGCCTA  
G L R P I V N M O Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
  
GCGGGCGGGGCCCCGGCTCTGGGCCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTCGTGCCTGGGTGCGGGCCAGGACCCGCCCTGAGCTGTACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
  
TGTCAAGGTGGATGTGACGGGCGGTACGACCCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGGTATGCCGTGGTCCA  
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P O N T Y C V R R Y A V V Q  
  
GAAGGCCGCCATGGGACGTCGCAAGGCCCTCAAGAGCCACGTCTACCTGACAGACCTCCAGGCGACATGCCACAGCTGCGTGGCTACCTGCAGGAGACCAGCCGCTGAGGGA  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
  
TGCGTGTGTCATGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGTCTCCACGTTCTGACGCTCATGTGCCACGCCGTGCCATCAGGGCAAGTCTACGTCA  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
  
CCAGGGGATCCCGAGGGCTCCATCCTCTCCACCTGCTGCAGGCTGTGACGGGACATGGAGAACAGCTGTTGGGGGATTGGGGGACGGCTGCTCTGCCTGGTTGGGA  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
  
TGATTTCTTGTGGTACACCTCACCTCACCCACCGGAAACCTTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGGTGAACCTGCGGAAGAACAGTGGTGA  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
  
TGAGAAGACGAGGCCCTGGTGGCACGGCTTTGTTAGATGCCGCCACGGCTATTCCCTGGTGGCCCTGCTGCTGGATACCCGGACCCCTGGAGGTGAGAGCGACTACTCCAG  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
  
CTATGCCGCCACCTCCATCAGAGCCAGTCTCACCTCAACCCGGCTCAAGGCTGGGAGGAACATGCCGAAACTCTTGGGTCTGCGCTGAAGTGTACAGCTGTTCTGG  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
  
TTTGCAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAAGATCCTCTGCTGAGGCTACAGTTCACTGCTGCTCCAGCTCCATTCTACAGCAAGTTGGAAAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N  
  
CCCCACATTCTGCGCTCATCTGACACGGCTCCCTCTGCTACTCCATCTGAAAGCCAAGAACGAGGGATGCGCTGGGGCAAGGGCGCCGCCCTGCTCCCTGG  
P T F F L R V I S D T A S L C Y S I L K A K N A E  
  
CCGAAGAAAACATTCTGCTGACTCCTGGGTGCTGGTC  
E E N I L V V T P A V L G S  
  
GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGCAGCTTCCGGTGTCTGGAGGGAGTTGGCTGGCTGTGACTCCTAGCCTCTGTTCCCCAG  
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L \*

Fig. 11N

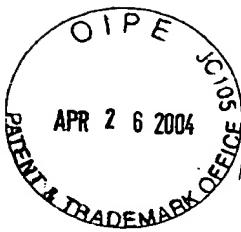


Protein that lacks motif A

APR 26 2004

ATGCCGGCGCTCCCCGCTGCCAGGCCGTGCCCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCACGTCGGCCACGGCCGCCCCCGCCG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCCGGGGACCCGGCGCTTCCCGCGCTGGTGCCAGTGCCTGGTGTGCGTGCCCTGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V O R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCCCTCTCCGCCAGGGTGTCCCTGCCAGAGGAGCTGGTGGCCCGAGTGCAGAGGCTGTGCCAGGCCGGCGAAGAACGTCGCTGGCTTCGCCGCTGGACGGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTCCGAGCTACCTGCCAACACGGTACCGCACGCACTGCCGGGGAGCGGGCGTGGGGCTGCTGCTGCCGCGTGGCGACGACG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTACCTGCTGGCACGCTGCCGCTCTTGCTGGTGCTCCAGCTGCCAACAGGTGCGGGCCGCCGCTGACGCTGCCGCTGCCACTCAGGCCGCCCCCGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGGGACCCGAAGGCCTGGATGCGAACGGCTGGGATGCGAACGGCTGGAAACCATAGCTCAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCCCGGTGCAGGAGGCCGGGGCAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCGTTGCCAACAGGCCAGGGCTGGCTGCCCTGAGCCGGAGGCCGGCCTGGCAGGGGCTCTGGGCCACCCGGCAGGACCCGGTGGACCCAGTC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGTTGCTACCTGCCAGACCCGCCAGAACAGCCACCTTGGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGGCCGCCAGCACACGCCGGCCCC  
G F C V V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATGCCGCCACACGCCCTGGACACGCCCTGTCCTGGAGACCAAGCAGCTTCTACTCTCTAGGCAGAACAGGAGCAGCTGCCCTCTTCTACTCAG  
S T S R P P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTCGTGGAGACCATCTTCTGGGCTCAGGGACTCCCGCAGGTTGCCCTGCCAGGCCACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGAAACACGCCAGTCCCCTACGGGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGGCCACTGGCA  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGGAGGGACACAGACCCCGTCCCTGGTGAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGGCTCTGGCC  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCTCCAGGACACAGACCCCGTCCCTAGGAACACCAAGATCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAGATGAGCGTGGGACTGCCCTGGCTGCCAGGAGGCCAGGGTTGGCTGTTCCGGCCAGCACCGCTGCCAGGAGATCTGGCAAGCTCGCTGCCAGGAGC  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTGTCAGCTGGAGCTGCCCTGGCTGCCAGGAGGCCAGGGTTGGCTGTTCCGGCCAGCACCGCTGCCAGGAGATCTGGCAAGCTCGCTGCCAGGAGC  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 110



AATCAGACAGCACTGAAAGGGTGAGCTGCCAGACGCTCGGAAGCAGAGGTAGGCAGCATCGGAAGCCAGGCCCCCTGCTGACGTCAGACTCCGCTCATCCCCAAGCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D  
CGGGCTGGGGCCGATTGTGAACATGGACTACGTCTGGAGCCAGAACCTCCGAGAGAAAAGAGGCCAGGGCTCCTCGAGGGTGAAGGCAGTGTCAAGGTGCTCAACTACGA  
G L R P I V N M O Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E  
GGGGCGGGCCGCCCCGGCTCTGGGCCTCTGTGCTGGCCTGGACATATCCACAGGGCTGGCGACCTTGTGCTGGGTGCGGGCCAGGACCCGCCCTGAGCTGACTT  
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F  
TGTCAAG GAGGGCTCACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGGTATGCCGTGGTCCA  
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q  
GAAGGCCGCCATGGCACGTCCCAAGAGCCACGTCTCACCTGACAGACCTCCAGCCGACATGCCACAGGGCTGGCCTACCTGCAAGGAGACCCGCTGAGGG  
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D  
TGCGTCTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGCTTCTACGCTCATGTGCCACACGCCGTGCCATCAGGGCAAGTCTACGTGACTG  
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C  
CCAGGGATCCGCAGGGCTCCATCTCCACGCTGCTGAGGACATGGAGAACAGCTGTTGGGGATTGGGGACGGGCTGCTCTGCCTGG  
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D  
TGATTTCTTGTGGTGAACCTCACCTCACCCACGCAGAACCTCTCAGGACCTGGTCCGAGGTGCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCC  
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P  
TGTAGAAGACGAGGCCCTGGTGGCACGGCTTTGTCAGATGCCGCCACGCCATTCCCTGGTCCGAGGTGCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCC  
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S  
CTATGCCGGACCTCCATCAGAGCCAGTCTCACCTCAACCGCGCTCAAGGCTGGAGGAACATGCGTCGAAACTCTTGGGTCTTGGCTGAAGTGTCAAGCTGTTCTGGA  
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D  
TTTGCAGGTGAACAGCCTCAGACGGTGTGACCAACATCTACAAGATCTCTGCTGAGGCTACAGTTACGCATGTGCTGCAGCTCCATTCACTACCAAGTTGGAGAA  
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N  
CCCCACATTTCTGCCGTATCTGACACGCCCTCCCTGCTACTCCATCTGAAAGCAAGAACGAGGGATGCGCTGGGGCAAGGGCGCCCTGCCCC  
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E  
GGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACGGTGTACCTACGTGCCACTCCTGGGTACTCAGGACAGCCAGCCAGCTGAGTGGAAAGCTCC  
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P  
GGGGACGACCTGACTGCCCTGGAGGCCAGCAACCCGGCACTGCCCTGAGCTCAAGACCATCTGGACTCATGCCACCCGCCACAGCCAGGCCAGAGCAGACCCAGCC  
G T T L T A L E A A A N P A L P S D F K T I L D  
CTGTACGCCGGCTCTACGTCCCAGGGAGGGGGGGCCACACCGAGGCCACCGCTGGAGTGTGAGGCTGAGTGTGAGTGTGTTGGCCAGGGCTGCATGCGCTGAAGGCT  
GAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCCTTCACTTCCCCACAGGCTGGCGCTGGCTCCACCCAGGGCAGCTTCTCAC  
CAGGAGCCGGCTTCACTCCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTCACCCCTGCCCTGCCCTTGCCTCCACCCACATCCAGGTGGAGACCCCTGAGAA

Fig. 11P



GGACCCCTGGGAGCTCTGGGAAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGGAGGGACCCCTGCACCTGGATGGGGTCCCTGTGGGCAAATTGGGGGAGGTGCTGTGGGACTAA  
AATACTGAATATATGAGTTTCAGTTTGAA

*Fig. 11Q*



Truncated protein that lacks motif A

ATGCCGCGCGTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCCAGCCACTACCGGAGGTGCTGCCGTGCCACGTTGTGCGCTGGCCAGCCACGGCCGCCCCGCCG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCGTGGTGGCCAGTGCTGCGTGGTGTGCGTGCCTGGGACGACGGCCGCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCTCTTCCGCCAGGTGCTGCTGCCGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCAGGCCGCCGAAGAACGCTGCTGGCTTCGCCGCTGGACGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTTACCAACCGCGCAGCTACCTGCCAACACGGTGACCGACCCACTGCCGGGAGCCGGCGTGGGGCTGCTGCCGTGCCACTCAGGCCGGCCCCCG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTACCTGCTGGCACGCTGCGCCTTTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCGTGTACAGCTGCCGTGCCACTCAGGCCGGTGGGGCTGCTGCCACTCAGGCCGGCCCCCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGGGACCCGAAGGCCTGGGATCGAACGGCTGGGATCGAACGGCTGGGACCCATAGCGTCAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCCGGGTGCAGGGAGGCCGGAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCGAAGTCTGCCGTGCCAACAGGCCAGGCCTGGGCTGCCCTGAGCCGGAGCCGGACGCCCTGGGAGGGCTGGGCCACCCGGCAGGACGCCGTGGACCGAGTC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTTGCTGGTGTACCTGCCAGACCCCGGAAGAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGGCCAGCACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGCGGCCACCGCTGGGACCGCTGGTCCCCGGTACGCCAGACCCACTCCCTACTCCCTACTCCCTAGGCACAAGGAGCAGCTGCCCTCTTCTACTCG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S  
  
CTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTGTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCGCCAGCGCTACTGGC  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGGAACCACGCCAGTGCCTCAAGACGCACTGCCGTGCCAGCTGCCAGCAGGCCCTGGCAGGTGACGGCTTCGCTGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCAAGGGCTCTGGCGGCCAGGCCAGGGAGGACACAGACCCCGTCCGGTGCAGCTGCCAGCACGCCCTGGCAGGTGACGGCTTCGCTGCC  
E K P Q G S V A A P E E E D T O P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCGCCGCTGGTGCCTGCCAGGCCCTGGGCTCCAGGCACAACGAACGCCCTGGTGCAGCTGCCAGCACGCCCTGGCAGGTGACGGCTTCGCTGCC  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAAGATGAGCGTGCAGGACTGCCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGTGCAGGTGAGGAGATCCGGCAAGTCTGCACTGGC  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGTACGTGCGAGCTGCTCAGGTCTTCTTATGTCACGGAGACCACGTTCAAAGAACAGGCTTTCTACCGGAAGAGTGTGGAGCAAGTTGCAAGGATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11R

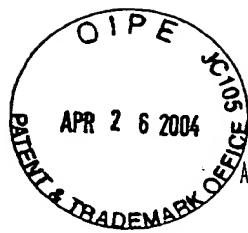


Fig. 11S



Lacks motif A and altered C-terminus

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCCCTCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGCCACGTTGTC  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGCGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGTTCCGGCGCTGGTGGCCAGTGCCTGGTGTGCCCTGGGACGCACGGCCGCCCCCGCCGC  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
CCCCCTCCTCCGCCAGGTGCTCCTGAAGGAGCTGGTGGCCAGTGCAGAGGCTGTGCAGGCCGCGAAGAACGTGCTGGCCTC GCCGCTGCTGGACGGGCCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACCGTGCAGCTACCTGCCAACACGGTACCGACGCCTGGGGAGCGGGCGTGGGGCTGCTGCCGCGTGGGACGACGT  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTACCTGCTGGCACCGTGCAGCTGGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGCCCCCGCC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGGGACCCGAAGGCCTGGGATCGAACGGCCTGGAACCATAGCGTACGGAGGCCGGTCCCCCTGGGCCTGCCAGCCCCGGTGCAGGGAGGCCGGCAGTC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCGTGCCAACAGGCCAGGCCTGGCGCTGCCCTGAGCCGGAGCCGACGCCCTGGCAGGGCTGGGCCACCGGGCAGGACCGTGGACCGAGTGC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAAGAGCCACCTTTGGAGGGTGCCTCTGGCACGGCCACTCCACCCATCCGGCCGCCAGCACACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
ATCCACATCGGGCACCCACGCTCCCTGGGACACGCCCTGGTACGCCAGACCAAGCACTCCCTACTCCCTAGGCACAAAGGAGCAGCTGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
CTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTGTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGCCTGCCAGCGTACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGCCGCCCTGTTCTGGAGCTGCTGGAAACCACGCCAGTGCAGTCCCTACGGGGTCTCTCAAGACGCAGCCGCTGCCAGCTGGCACCCAGCAGGGTGTCTGCC  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCCAGGGCTCTGGCGGCCAGGAGACAGACCCCGTGCCTGGCAGCTGCCAGACAGACCCCTGGCAGGTACGGCTCTGCCAG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCTGGCTGGTGCCTGCCAGGCCCTGGGCTCCAGGCACACGAACGCCCTCCAGGAACCCAAGAAGTCTCCCTGGGAAGCATGCCAGCTCGCTGCCAG  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L  
  
GACGTGGAAAGTGGCGTGGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGCCAGAGCACCGTCTGCCAGGGAGATCTGGCAAGTCTGCCACTGGC  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
  
GATGAGTGTGACGTGTCAGCTGCTAGGTCTTCTTATGTCAGGAGACACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTGGAGCAAGTGTCAAG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T



ATCACACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGCGAACAGAGGTAGGGAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCAGACTCCGTTCATCCCCAACCTGA  
 IRQHLKRVQLRELSEAEVROHREARPALLTSRLRFIPKPD  
 CGGGCTGCGGCCATTGTGAAACATGGACTACGTGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCACTGTTAGGGTCAACTACGA  
 GLRPIVNMODYVVGARTFRREKRAERLTSRVKALFSQLNYE  
 GCGGGCGCGGCCGCCCCGGCCTCTGGCGCCTGTGCTGGCCCTGGACGATATCACAGGGCCTGGCGACCTTCGTCGCTGCGTGTGCGGGCCAGGACCCCCCCTGAGCTGACTT  
 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPPELYF  
 TGCAAG GACAGGCTACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTAACGCTGCGTGTGCGTATGCCGTGGTCA  
 VK DRLTEVIASIICKPQNTYCVRRYAVVO  
 GAAGGCCGCCATGGCACGTCGCAAGAGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCGACAGTCGTCGCTCACCTGAGGGACAGCCGCTGAGGG  
 KAAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD  
 TGCGCTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTCGACGCTTCACGCTCATGTGCCACACGCCGTGCGCATAGGGCAAGTCACGTCAGTG  
 AVVIEQSSSLNEAASSGLFDVFLRFMCHHAVRIRGKSYVQCG  
 CCAGGGGATCCCGCAGGGCTCATCTCCACGCTGCTGAGCCGACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCGTTGGTGA  
 QGIPQGSILSTLLCSLCYGDOMEENKLFA  
 TGATTTCTTGTGGTACACCTCACCTACCCACCGCAGAACCTCCCTGAGGACCTGGCTGGTCCAGGCTGAGTGGCTGGTGAACCTGCGAACAGTGGTGAACCTCC  
 DFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFP  
 TGAGAACGAGGCCCTGGTGGCACGGCTTGTTCAGATGCCGCCCCACGGCTATTCCCTGGCGCCCTGCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG  
 VEDEAALGGTAFVQMPAHGLFPWCGGLLDTRTLEVQSDYSS  
 CTATGCCGACCTCCATCAGAGCAGTCACCTCAACCGCCGCTCAAGGCTGGAGAACATGCGTCGAAACTCTTGGGTCTTGGCTGAAGTGTACAGCTGTTCTGGA  
 YARTSIRASLTFNRGFKAGGRNMRRKLFEGVLRLKCHSFL  
 TTGAGGTGAACAGCCTCAGACGGTGTGACCAACATCTACAAGATCCTGCTGAGGCTGAGGTTACGGTACGCTGCTGCTGAGCTCCATTTCATCAGCAAGTTGGAAGAA  
 LQVNLSLQTVCTNIYKILLLQAYRFHACVQLQLPFHQQVWKN  
 CCCCACATTCTCGCGCTCATCTGACACGGCCCTCCCTGCTACTCCATCTGAAAGCCAAGAACGCCAGGGATGCGCTGGGGCCAAGGGCGCCGCCCTGCCCCCGA  
 PTFFLRVISDTASLCYSILKAKNAE  
 CCGAAGAAACATTCTGCTGACTCTGCGGTGCTGGT  
 EENILVVTPTPAVLGS  
 GGGACAGCCAGAGATGGAGCCACCCCGAGACCGTGGGTGAGCTTCCGGTGTCTGGAGGGAGTTGGCTGGCTGTGACTCCTCAGCTGTTCCCCAG  
 GQPEMEEPPTRRPSGVGSFPVSPGRRGVGLGL\*

Fig. 11U



Truncated telomerase (ver. 2)

ATGCCGCGCGCTCCCGCTGCCAGCGCTCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGGCACGCGCCACGTCGT  
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
 CGGCCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGACCCGGCGCTTCCCGCGCTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGACGGCCGCCCCCGCCG  
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
 CGCCTCCCCGGGTCGGCGTCCGCTGGGTTGAGGGCGCCGGGGAAACCGCAGCATGCCAGCGACTCAGGGCGCTCCCCCGAGGT  
 G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
 A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
 CCCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCGAGCCGGCGCGAAGAACGTGCTGGCCTGGCTTGCGCTGGACGGGGCCG  
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
 CGGGGGCCCCCGAGGCGCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGGCTGCTGCGCCGCTGGGACGACG  
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
 GCTGGTTCACCTGCTGGCACGCTGGCGCTTTGTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCGCCGCTGTACAGCTGGCGCTGCCACTCAGGGCGCTGGACGGGGCCG  
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
 ACACGGTAGTGGACCCGAAGGGCTGGATGCAACGGGCTGGAACCATAGCGTCAGGGAGGGGGTCCCCCTGGCCTGCCAGCCCCGGTGCGAGGAGGGCGGGGAGTGC  
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
 CAGCCGAAGCTGCCGTGCCAACAGGGCCAGGCCTGGCGCTGCCCTGAGCCGAGGCCGCTGGCAGGGGCTGGGCCACCCGGCAGGACCCGTGGACCGAGTGC  
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
 TGGTTCTGTGTTGTCACCTGCCAGACCCCGAAGAAGCCACCTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGGCCACCCACCGCAGGGGGCC  
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
  
 ATCCACATGCCGCCAACACGCTCCGGACACGCCCTGTCCCCGGTACGCCAGACCAAGCACTCCCTACTCCCTAGGCAGACAAAGGAGCAGCTGCCCTCCCTACTCAG  
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S  
  
 CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGCCTGCCAGCGCTACTGGCA  
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y H Q  
  
 AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGCGCAGTGCCTACGGGTGCTCTCAAGACGCAGCTGCCCTGCCAGGGTGCCTGCCAGCGCTACTGGCA  
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
 GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGAGGAGCACAGACCCCGTGCCTGGTGAGCTGCCAGACAGCAGGCCCTGGCAGGGTACGGCTCGCGGGCTG  
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
 CCTGCCGCCCTGGTGCCTCCAGGCCTCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACCAAGAAGTCATCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGC  
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11V



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTGGCTGCGCAGGGAGCCAGGGGTTGGCTGTTCCGGCGCAGAGCACCGTCTCGTGAGGAGATCCTGGCCAAGTTCCCTGACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGTGACGTGTCGAGCTGCTCAGGTCTTCTTATGTACGGAGACCAAGCTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AAT--NNN--GACAGTCACCAGGGGGTTGACCGCCGGACTGGGCTCCCAGGGTTGACTATAGGACAGGTGTCCAGGTGCCCTGCAAGTAGAGGGCTCTAGGGCTGGCTGG  
CATGGGTGGACGTGGCCCCGGCATGGCCTCTCGCTGCTGCCGTGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGCTTGTGGCTTCCGTGAGCTTCCCTAGTCTGTTGCTG  
GCTGAGCAAGCCTCCTGAGGGCTCTATTG...

*Fig. 11W*



Truncated protein 1 (ver. 2)

ATGCCCGCGCTCCCGTGCCGAGCCGTGCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGGCACGTCG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGCGCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCTTCCCGCCTGGTGGCCAGTGCCTGGTGC  
R R L G P O G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
GGCTCCCCGGGTGGCGTCCGGCTGGGTTGAGGGCGCCGGGGAAACAGCGACATGCCAGAGCAGCGCAGCGACT  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P O V  
  
CCCCCTCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCAGAGGCTGTGCAGCGCCGGCGAAGAAC  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACAGCGTGGCAGCTACCTGCCAACACGGTGACCGACGC  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
GCTGGTTACCTGCTGGCACCGCTGCCGCTTTGCTGGTGGCTCCAGCTGCCCTACAGGTGCGGGCCCGC  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
ACACGCTAGGGACCCGAAGGGCTGGGATGCAACGGCCTGGAACCATAGCGTCAAGGGAGGCCGGT  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
CAGCCGAAGCTGCCGTGCCAACAGGCCAGGGCTGGCGCTGCCCTGAGCCGAGCCCGTGGCAGGG  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
TGGTTCTGTTGGTCACCTGCCAGACCCGCCAGAGAACGCCACTTGGAGGGTGCCTCTGCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P  
ATCCACATCGGGCACCGCTGGACACGCCCTGCCCCGGTACGCCAGAACACTCTCTACT  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S  
CTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGTGGAGACCAT  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
AATCGGGCCCTGTTCTGGAGCTGCTGGAACCAACGCCAGT  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
GGAGAAGCCCCAGGGCTCTGGCGCCGGAGGGACACAG  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
CCTGCAGGGCTGGTGCCTGGGCTCAGGCACA  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11X



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCGCAGAGCACCCGCTGCGTGAGGAGATCCTGGCCAGTTCTGACTGGCT  
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L  
GATGAGTGCTACGTGTCGAGCTGCTCAGGTCTTCTTTATGTCAAGGAGACCAAGCTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG  
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G  
AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGCGGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCGCTGCTACGTCCAGACTCCGCTCATCCCCAAGCCTGA  
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTGGTTAACCTCTTTAACAGAA  
V A V L W F T F L F N Q K

CGGGCTGCCGATTGTGAACATGGACTACGTGCGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTAGCCTGCTCAACTACGA  
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G \*

*Fig. 11Y*



Truncated protein 2 (ver. 2)

ATGCCGCCGCTCCCCCTGCCAGCCGTGCCCTCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGCCACGTTGTG  
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V  
  
CGGCGCTGGGGCCCCAGGGCTGGCGCTGGTCAGCGGGGACCCGGCGCTTCCGCCGCTGGTGGCCAGTGCTGGTGTGCCGCTGCCCTGGGACGCACGGCCGCCCCCGCCG  
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A  
  
GGCCTCCCCGGGTCCGGCTCGGCTGGGTTGAGGGCGGCGGGGGAACCGCAGCATGCCAGAGCAGCAGCCAGGCACTCAGGGCGCTCCCCCGAGGTG  
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R  
A S P G S A S G W G \* G R P G G T S D M R R A A Q A T Q G A S P A G  
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V  
  
CCCCCTCCGCCAGGTGTCCCTGCCCTGAAGGAGCTGGTGGCCAGTGCTGCCAGAGGTGTGCCAGGCCGCGAAGAACGTGCTGGCCTTCGCCCTGCCCTGCCCTGGGACGGGCG  
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R  
  
CGGGGGCCCCCGAGGCCTCACCAACCGTGCAGCTACCTGCCAACACGGTACCGACCGACTGCCGGGGAGCGGGGGCTGGGGCTGCTGCCGCCGCGTGGGACGGGCG  
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V  
  
GCTGGTTCACCTGCTGGCACCGCTGCCGCTTTGCTGGCTCCAGCTGCCCTACCGGTGTGCCCTACCGAGCTGCCAGCTCGGGCCGCCGCTGTACAGCTGCCGCTGCCACTCAGGGCCGCCCCCG  
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P  
  
ACACGCTAGTGGACCCGAAGGGCTCTGGGATCGAACGGGCTTGGAACCATAGCGTCAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCGGTGCAGGAGGCCGGAGCTGC  
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A  
  
CAGCCGAAGTCTGCCGTTGCCAACAGAGGCCAGGGCTGGCGCTGCCCTGAGCCGGAGCCGGTGGGGCAGGGGCTGGGCCACCCGGCAGGACCGTGGACCCGAGTGC  
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R  
  
TGGTTCTGTGGTGTACCTGCCAGCCGCCAACAGAGCCACTTGGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTGGGCCAGCACACGCCGGCCCC  
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H A G P P  
  
ATCCACATCGGGCACCGCTCCCTGGACACGCCCTGGCTCCCGGTGACCCGAGAACACTCCCTACTCCTCAGGCAGACAGGAGCAGCTGCCCTCCCTACTCAG  
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S  
  
CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGTGGAGACCATTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCCTGCCAGGCCACTGGCA  
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q  
  
AATGGGGCCCTGTTCTGGAGCTGCTGGGAACCACGCCAGTCCCCAACGGGGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGGAGCTGCCAGGCCACTGGCA  
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R  
  
GGAGAAGCCCCAGGGCTCTGGCGGCCCGAGGGAGGGACACAGACCCCGTCGCCCTGGTCAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGGCTCGTGCGGCC  
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C  
  
CCTGCCGCCGCTGGTGGCCCAAGGCCCTGGGCTCAGGCACAACGAACGCCGCTCTCAGGAACACCAAGAAGTCATCCCTGGGAAGCATGCCAGCTCGTGCGAGGCT  
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11Z